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January 14, 2004, 15:52:50; Search time 1784.1 Seconds (without alignments) 8323.656 Million cell updates/sec
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1 caggttactctgaaagagtc.....cctcagtcaccgtctcctca 363
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10:0 , Gapext 1.0
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Maximum DB seq length: 200000000
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gb_htg:

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	97 M.musc	152 Sequence	U22977 Mus mus	7.6250	U22992 Mus muscul	E07584	U23010 Mus muscul	U23013 Mus	U2300	E07990 DNA enco	145910 Sequence	U2300Z	U22984 Mus muscul	U230	U22997 Mus	XS309	U23007 Mus	V PI 788578	022329 AR026944	m. W 86052X	505250	U22911 Mus mu	U22926	U22958 1	AC073939 Mu	02298 112398	S82427 anti-p	U22955 Mus mi	/ AD4218// Mus S63186 Ig VH=	U22990 Mus	U22975 Mus m	U22907 Mus muscul	ENTS		p mRNA linear ROD 23-FEB-1994 Bl antibody heavy chain variable	egion.	Vertebrata; Euteleostomi	Schurognathi: Muridae: Murinae: Mus.
	a	720	Ŋ	<u></u>		9	q	9 1	MMU23013	9 9	Į,	145910	MMT23002	MMU22984	MMU23005	MMU22997	MMIGMSMJ	MMU23007	875897	MM022929	MMHCVR4	MM022905	MMU22911	MMU22926	MMU22956	AC073939	MMU22988	S82427	i Si	`	•	MMU22975	2290	ALIGNMENTS		360 bp NA for ASWB:	ion; VH use)	ata;	. q.
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% Query	Match	87.2																																		MMHCVR3 M.musculus	ion. 097 097.1 ibody; muscul	muscu arvota	. 4. 4.
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<1. .>420

/note="VDJ region"
/codon start=1
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IgM heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                   Zu(bases 1 to 420)
Xu,H., Sharma,A., Chen,L., Harrison,C., Logan,J.S. and Byrne,G.W.
Direct Submission
Submitted (2.10-MAR-2002) Immunology, Nextran Inc., 303B College Road
East, Plainsboro, NJ 08540, USA
Location/Qualifiers
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Li (bases I to 420).

Xu, H., Sharma, A., Chen, L., Harrison, C., Wei, Y., Chong, A.S., Logan, J.S., Byrne, G.W. and Shama, A.

In structure of anti-dal immunoglobulin genes in naive and stimulated Gal knockcut mice

Transplantation 72 (11), 1817-1825 (2001)
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/mol type="mana"
/db xref="taxon:10090"
/clone="GN-2-M4"
/cell type="hybridoma"
/note="generated in alpha-1,3-galactosyltransferase
knockout mice"
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                                                                     Mus musculus (house mouse)
                      GI:20177160
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AUTHORS
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JOURNAL
ACCESSION
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                                                                                                                                                Direct Submission
Submitted (09-SEP-1993) M. Monestier, Center for Molecular Medicine
and Immunology, one Bruce Street, Newark, NJ 07103-2763, USA
Location/Qualifiers
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KGLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYYCARVDG
YYDAMDYWGQGTSVTVSS"
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Mus musculus clone GN-2-M4 monoclonal
anti-alpha-1,3-galactosyltransferase IgM heavy chain mRNA, partial
cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="ASWB1 heavy chain variable region"
'protein id="CAA52988.1"
'db_xref="G1:414166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .>360
/gene="VH ASWB1"
/product="ASWB1 heavy chain variable region"
1 95 c 89 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 316.6; DB 10; Length
Pred. No. 1.6e-91;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="ASWB1 hybridoma"
/cell_type="hybridoma"
[. .360
                J. Immunol. 152 (2), 667-675 (1994)
94110621
8283044
                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VH ASWB1"
<1. .>360
/gene="VH ASWB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
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ilarity 93.9%;
Conservative
                                                                                                   2 (bases 1 to 360)
Monestier, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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     H-2S mice
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Best Local Simil
Matches 341; (
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180 240 240 300 299

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/ organisms "wise musculus"
/mol_type="mRNA"
/strain="TBT7 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-11h"
/clone="45-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 cadocificadaaadddicigaagigacigacacacafiffacigagaigafgacaagcac 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICCICAAGAICACCAGIGIGGACACICGAGAIACIGCCACAIACIACIGIGCICGAAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GICTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 360)
                                                                                                                                                                                                                                                                              Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 305.4; DB 10;
Pred. No. 7.2e-88;
0; Mismatches 26; I
                                                                                                                                                                                                                                                                                                                                                 Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)
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                                                                                                    Mus musculus (house mouse)
Mus musculus
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92.0%;
                                     GI:780556
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                                     U22977.1
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Best Local S:
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/protein id="CDD38347.1"
/brotein id="CDD38347.1"
/db xref="C1:217240903"
/translation="MDRLTSSFLLIUPAYVLSQATLKESGPGILQSSQTLSLTCSFSGRSLSTSGMGYGWIPERGPSGRGJEWLAHIYWDDDKRYNPSLKSRLTISKDTSRRQVFLKISVDPADTATYYCVRRPITPVLVDAMDYWGQGTSVTVSS"
                                                                                                                                                PAT 08-JUL-2002
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                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Nus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Humanized antibodies that recognize beta amyloid peptide
Patent: WO 0246237-A 15 13.JUN-2002;
Neuralab Limited (BM); Wyeth (US)
Location/Qualifiers
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Pred. No. 6e-90;
0; Mismatches 22; Indels 6;
                                                                                                                                                linear
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                                                                                                                                                    DNA
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                                                                                                                                            AX458152 426 bp Sequence 15 from Patent WO0246237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:10090"
1. _>426
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Best Local Similarity 92.4%;
Matches 341; Conservative
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Pred. No. 7.2e-88;
0; Mismatches 26; Indels 3;
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/strain="CB17 SCID"

/sub species="domesticus"

/db xref="taxon:10090"

/clone="45-27b"
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Int. Immunol. 7 (5), 807-819 (1995)
96053543
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/tissue_type="spleen"
<1. .>360
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Mus musculus
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Best Local Similarity 92.0%;
Matches 334; Conservative
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/protein_id="AAA96360.1"
/brotein_id="G1:780561"
/branslation="G1:780561"
/translation="G7TLKESGPGILQSSQTLSLTGSFSGFSLSTSGWGVSWIRQPSG
KGLEWLAHIYWDDDXRYNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYYCARRAL
           360 bp mRNA linear ROD 09-APR-1996
Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
Clone 45-12h, partial cds.
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Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSWB 2.137,
Houston, TX 77030, USA
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Best Local Similarity 92.0%; Pred. No.<sup>7</sup>7.2e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3;
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/mol type="mRNA"
/strain="CB17 SCID"
/sub species="domesticus"
/db xref="taxon:10090"
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/tissue_type="spleen"
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Young, D.C.
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/codon_start=1
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/db_xref="d1:780591"
/tb_xref="d1:780591"
/db_xref="d1:780591"
/db_xref="d1:78
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Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
2008 45-27h, partial cds.
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Direct Submission (17-MRR-1995) David C. Young, University of Texas Health Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137, Houston, TX 77030, USA
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Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
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C12P21/08,C07K15/28//C12N15/06,C12N15/13,C12N15/62,G01N33/569,
                                          TATAACCCATCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA 240
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Gene fragment coding the variable region in the heavy chain.
E075B4
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Tokiyoshi,Y.
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topology: Linear;
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Pred. No. 2.8e-87;
0; Mismatches 29
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Patent: JP 1994141885-A 1 24-MAY-1994;
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/organism="Mus sp."
/mol type="genomic RNA"
/db_xref="taxon:10095"
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strandedness: Double;
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JP 1994141885-A/1
24-MAY-1994
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Best Local Similarity 91.3%;
Matches 334; Conservative
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JP 1994141885-A/1.
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/product="immunoglobulin heavy chain"
/protein_id="haAa6373.1"
/db_xref="Gi:780587"
/tb_xref="GYTLKESGPGILQSSQTLSLTCSFSGFSLSTSGWGVSWIRQPSGKGLEMLAHIYMDGDKRYNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYYCARRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
Location/Qualifiers
                                   241 TICCICAAGAICACCAGIGIGGACACIGCAGAIACIGCCACAIACIACIGGCCCGAAGA 300
                                                                             301 GICTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGGTCACCGTCTCC 360
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TICCTCAAGAICACCAGIGIGGACACICGAGAIACIGCCACAIACIGCGIGGIGCICGAAGG 300
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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Pred. No. 2.4e-87;
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Mus musculus
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Best Local Similarity 91.7%;
Matches 333; Conservative
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/mol type="mmNA"
/strain="CB17 SCID"
/sub species="domesticus"
/db_xref="taxon:10090"
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Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-13h, partial cds.
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Solience Center, Marston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Young, D. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of Ig
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Pred. No. 2.6e-86;
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Best Local Similarity 91.2%;
Matches 331; Conservative (
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/dine=145-6h"
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Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-6h, partial cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequence analysis and antigen binding characteristics of Ig
Ig+ mice
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Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Submitted (17-MAR-1995) David C. Young, University of Science Center, Houston, Pathology, 6431 Fannin, MSMB Houston, TX 77030, USA
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יהיטלבטטן מל 151 bp mRNA linear ROD 20-SEP-2001
Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-3h, partial cds.
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Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
Location/Qualifiers
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                                                                                                                                                                                                       DB 10; Length 360;
                                                                                                                                                                                                                                                                                 29; Indels
                                                                                                                                                                                                   Score 300.6; DB 1
Pred. No. 2.6e-86;
0; Mismatches 29
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/organism="Mus musculus"
/nol_type="maxx"
/strain="CB17"
/sub_species="domesticus"
/db_xref="taxon:10090"
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/tissue_type="spleen"
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Mus musculus
                                                                                                                                                                                              Query Match 82.8%;
Best Local Similarity 91.2%;
Matches 331; Conservative (
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2 (bases 1 to 361)
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/translation="QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSG
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Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77036, USA
Location/Qualifiers
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 360)
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        Pred. No. 2.6e-86;
; Mismatches 29;
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Corganism=Mus musculus"

/mol.type="mRNA"

/strain="CB17 SCID"

/sub species="domesticus"

/db xref="caxon:10090"

/clone="45-8h"
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tissue_type="spleen"
11. .>360
Best Local Similarity 91.2%; Pr.
Matches 331; Conservative 0;
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/cell_type="lymphocyte"
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PF 17-EEB-1993 UP 1993028173
PI SHIMAMURA TOSHIAKI, NAKAZAWA HARUMI, HAMURO JUNJI PC C12N15/12, A61K37/02, C12N15/70, C12P21/02; CC C topolomy in the constant of the constant of
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DNA encoding inhibitor of binding IL-6 to its receptor
E07990
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Shimmamura, T., Nakazawa, H. and Hamuro, J.
INWUNOSUPPRESSANT
Patent: JP 1994237772-A 1 30-AUG-1994;
AJINOMOTO CO INC
OS Unknown
PN JP 100-100
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t
/strain="CB17 SCID"
/sub_species="domestic
/db_xref="taxon:10090"
/clone="45-2h"
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   <1. .>361
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KGLENTHINGSDRKYNPSLKSRLTISKDTSRNQVFLRITSVDTADTATYYCARRAL
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Young, D.C.
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                                             /cell type='hybridoma'
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peptide 1. 738
/product='inhibitor of binding og IL-6 to its
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Matches 335; Conservative 0; Mismatches 28; Indels
                                      organism='Unclassified'
Location/Qualifiers
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Shimmamura,T., Nakazawa,H. and Hamuro,J.
Immunosuppressant
Patent: US 5639455-A 6 17-JUN-1997;
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a 189 c 180 g 182
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Description	urine Mab 1F7	le Mab 1F7	MAb 3B9 h	chain var	chain cod	ric antibo	chain var	Chimeric 3B9 monoc
			Descri	Murin	Murir	Mouse	Heav	Heav	Chime	Heav	Chime
SUMMARIES			ΩI	AAL48651	AAL48652	AAQ83491	AAX85885	AAX79520	AAQ83492	AAX85886	AAX79542
			99	24	24	16	20	20	16	20	20
	•		Match Length DB	363	363	483	483	483	423	423	423
	40	Query	Match	100.0	100.0	86.3	86.3	86.3	85.9	85.9	85.9
		•	Score	363	363	313.4	313.4	313.4	311.8	311.8	311.8
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Mouse 10D5 VI Humanised MA	112 Il-6 bi	00 Murine anti	99 Murine	89 Mouse Meavy	0.00	41 Humanised 10D	00 DNA encoding	00 DNA sequence #1	46	99	56 Rat immun	7.9	00 Rat activ	3.7	06	σ	27 Antibody Bl	10	7	3 Human immu	16	19	1 Monoclonal antil	7 Anti-h	4 Human immunogl	Human Human	61 DNA encoding mc	54 Human anti-HIV	33 Human secreted	48 Human immunoglo	93 Humani	87 Неалу	
ABS594	~	AAT093	AATO92	ARN846		ABZ246	ABK110	AAS145	AAA 996	AAQ641	AAQ370	AAX994	AAA510	AAQ454	AAH423	AAQ455	AAZ394	AAZ239	AAX7920	m	AAQ759	AAC665	0	IO.	m	\sim	\sim	ABA085	AAC000	AAQ789	AAQ834	AAX858	1000
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ALIGNMENTS

RESULT 1

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Mouse, 1F7, antibody, immune modulator, anti-HIV antibody, CDR, complementarity determining region, framework-determining region; FR, heavy chain, light chain; HIV infection; gene; ss.
                                                               Murine Mab 1F7 heavy chain coding sequence.
       BP.
                                                                                                                                                                           11-JAN-2002; 2002WO-US00927.
        AAL48651 standard; DNA; 363
                                                                                                                                                                                             11-JAN-2001, 2001US-0759112.
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                                                                                                                                                                                                               (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                  Kohler H;
                                                                                                                                                                                                                                                    WPI; 2002-590668/63.
                                                                                                                                       WO200255668-A2.
                                                                                                                                                         18-JUL-2002.
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                                                                                                                                                                                                                                  Muller S,
                          AAL48651;
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AAL48651
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New polynucleotide encoding a complementarity- or framework-determining

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18-JUL-2002
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                                                                    The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HTV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 heavy chain
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region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV
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                                                                                                                                                                         Length 363;
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                                                                                                                                                    Sequence 363 BP; 83 A; 100 C; 88 G; 92 T; 0 other;
                                                                                                                                                                         100.0%; Score 363; DB 24; 100.0%; Pred. No. 7.7e-102;
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'note= "no start or stop codon"
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Matches 363; Conservative
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The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CPR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 heavy chain
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100.0%; Pred. No. 7.7e-102;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 17-18; 27pp; English.
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11-JAN-2002; 2002WO-US00927
                                                 11-JAN-2001; 2001US-0759112
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                                                                                                     (IMMP-) IMMPHERON INC
                                                                                                                                                    Muller S, Kohler H;
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121 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin B-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes the heavy chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhintis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease, rhey are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain variable region cDNA of murine IL-4 antibody 3B9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating IL4-mediated conditions
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                                                                                                                                                                                                                                             AAX85885 standard; cDNA; 483
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93US-0117366.
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07-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells from mice immunized with human IL-4 were used to prepare omas, which were screened for anti-IL-4 {\rm MAD} secretion. Only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGGITACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hybridomas, which were screened for anti-IL-4 MAb secretion. Onlicino 389 was positive. CDNA closes of the 389 light and heavy chains were cloned into pGEMYF4 and transformed into E. coli DH5-alpha. The clones were sequenced (AAQ83490-91), and used for
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   Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
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93US-0136783.
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                                   DB 20; Length 483;
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                                                                         Indels
483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;
                                                                       31;
                                 Score 313.4; DB 2
Pred. No. 1.6e-86;
0; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ83492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ83492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allargic disorder; allergic rhintles; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; ss.
 ACTTGTTCTTTCTCTGGGTTTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTCGT 240
                                                                                                                                                 TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCCAAGGATACCTCCAGCAACCAGGTA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody of the invention. The antibody is a chimeric or minanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
                                                                                                                                                                                         TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG
                                                                                                                                                                                                                         TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACATACTACTGTGCTCGAAGA
                                                                                                                                                                                                                                                                 GTCTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                     GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGGGACCACGGTCACGGTCTCC
                                       CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC
                                                                           CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC
                                                                                                               TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the heavy chain of the murine 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain coding sequence for murine 3B9 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX79520 standard; cDNA; 483 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0483636.
93US-0117366.
93US-0136783.
94WO-US10308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant IL4 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gross MS, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-370482/31.
P-PSDB; AAY18121.
                                                                                                                                                                                                                                                                                                                                                                               TCA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5914110-A.
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AAX79520;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICCICAAGAICACCAGIGIGGACACICGAGAIACIGCCACAIACIACIGIGCICGAAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrccrcaagarcaccagreresacacrecagaracrecacacaracracrerereresaga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the heavy chain variable region of murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, acopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 311.8; DB 20; Length 423;
Pred. No. 4.8e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA molecules encoding recombinant antibodies useful treating IL4-mediated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Holmes SD, Sylvester DR;
                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 3; 50pp; English.
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91.2%;
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                                                                                                                                                    93US-0117366.
                                                            95US-0483632
                                                                                                                         95US-0483632
                                                                                                                                                                                                                    94WO-US10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-429500/36.
P-PSDB; AAY23769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCA 423
                                                            07-JUN-1995;
                                                                                                                         07-JUN-1995;
                                                                                                                                                    07-SEP-1993;
                                                                                                                                                                                                                       07-SEP-1994;
27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                  Gross MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heavy chain variable region cDNA of murine/human chimeric antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACTIGITCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 Trccrcaagarcaccagrargacacacragaracraccacaracracrargracragaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCCAGCAACCAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                      A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAD 3B9 variable region including 3 CDRs (AAR70198-200) and a human antibody signal peptide (AAR70193). The construct was used for humanized antibody production. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                       nal antibodies (mAbs), derived treatment of IL-4-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 311.8; DB 16; Length
Pred. No. 4.8e-86;
0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
                                                                                Chimeric and humanised IL-4 monoclonal from high affinity mAbs - useful in tre and IgE-mediated allergic conditions
                                                                                                                                                                                                                Disclosure, Fig.3; 97pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX85886 standard; cDNA; 423 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.2%;
Matches 331; Conservative
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Chimeric - Homo sa
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                       P-PSDB; AAR70191
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361 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCC 420
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Best Local Similarity 92.4%;
Matches 341; Conservative
                                                                                                                                                         ABS59429 standard; DNA; 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEURALAB LTD.
(AMHP ) WYETH.
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                                                                                                                                                                                                                                                   Mouse 10D5 VH gene
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                                                 TCA 363
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                                                                                                                                                                                        ABS59429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCC 360
                                                                                           Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic fullitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAAGGATACCTCCAGCAACCAGGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trecticaagarcaccagrefegacacrecagaracreccacaracracrecrescenceaga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the DNA encoding the light chain of the chimeric 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCCAAGGATACCTCCAGGAACCAGGTA
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                                                                  Chimeric 3B9 monoclonal antibody heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 311:8; DB 2
Pred. No. 4.8e-86;
0; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                        Sylvester DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 3; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                               95US-0483636.
93US-0117366.
93US-0136783.
94WO-US10308.
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91.2%;
                                                                                                                                                                                                                                                                     95US-0483636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant IL4 antibodies
                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gross MS, Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-370482/31.
P-PSDB; AAY18125.
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                                                                                                                                                                                                                                                                                                                            14-OCT-1993;
07-SEP-1994;
                                                                                                                                                                                                                                                                  07-JUN-1995;
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                                   11-AUG-1999
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The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 16/1005 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic fisase or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present nucleic acid sequence encodes a mouse 306/1005 variable light (VL) chain or variable heavy (VH) chain protein of the invention.
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Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGITACTCIGAAAGAGICIGGCCCIGGGATATIGCAGCCCTCCCAGACCCICAGICIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 11
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241 ITCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG
                                                                                                       298 TTCCTCAAGATCACCAGGGGGCCCTGCAGATACTGCCACATACTACTGTGTTCGAAGG
                                                                                                                                     GTC-----TCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACC
                                                                                                                                                            358 cccarracrccggracragrcgargcrarggacracrggggrcaaggaaccrcagrcacc
                                 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCCAAGGATACCTCCAGCAACCAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAQ68709-10 encode the heavy and light chains respectively of the humanised monoclonal antibody (MAD) of the invention. The antibody has the ability to neutralise human immunodeficiency virus. The antibody is classified as 1gG kappa and has the sequence RIGPGR or RVGPGR in the principal neutralising domain. The antibody may be used to neutralise the clinically separate strains which cannot be neitralised by the neutralising antibodies against IIIB and IIIMN strains.
                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; murine; heavy; light; chain; monoclonal; antibody; complementarity determining region; CDR; IgG; kappa; IIIB; IIIMN; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIINN antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                CDNA to mRNA; 366 BP.
                                                                                                                                                                                                                                                                                                                                                          Humanised MAb H-chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92JP-0322476
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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P-PSDB; AAR54101.
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1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGACTCTG 60

Query Match
83.6%; Score 303.6; DB 15; Length 366;
Best Local Similarity 91.3%; Pred. No. 1.5e-83;
Matches 334; Conservative 0; Mismatches 29; Indels 3;

Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 0 other;

Gaps

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180
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                                                 ACTTGTTCTTTCTCTGGGGTTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTCGA 120
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CAGGITACTCTGAAAGAGTCTGGCCCTGGTATATTGCAGCCCTCCCAGACCCCTCAGTCTG
                                                                    ACCIGITITICICITICACIGAGCACTITITICACIGAGCAGTATICGT
                                                                                                               CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC
                                                                                                                                              cadeerreadgeaadgricredadrederedeacacarrirarreggargardacadeac
                                                                                                                                                                                                                                             TICCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG
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                                                                                                                                                                               TATAACCCATCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis; septic shock; multiple myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ70612 codes for human interleukin-6 binding inhibitor, the polypeptide described in AARS6612. This polypeptide ihibits the binding of human IL-6 to its receptor, and can therefore useful in the treatment of a variety of autoimmune diseases; specifically in the treatment of rheumatoid architis, septic shock due to bacterial infection and multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its receptor - useful for treating auto:immune disease induced or aggravated by IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 19; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Il-6 binding inhibitor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamuro J, Nakazawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AJIN ) AJINOMOTO KK
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P-PSDB; AAR58612.
                                                                                                                                                                                                                                                                                                                                                                            TCCTCA 363
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                                                                                                                                       CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC
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                   Score 299.2; DB 15; Length 738; Pred. No. 4.4e-82;
                                       Indels
 Sequence 738 BP; 187 A; 189 C; 180 G; 182 T; 0 other;
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                                      28;
                                       0; Mismatches
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                 82.4%;
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                             Local Similarity
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murine anti-protein C monoclonal antibody HPC-4 heavy chain variable region (VH gamma). HPC-4 recognises the activation peptide region profess of the heavy chain of protein C, a vitemin K-dependent plasma protein zymogen. Protein C is activated to activated protein C (APC) by cleavage between the Arg-Leu amino acid contained within the activation peptide sequence. HPC-4 prevents protein C activation to APC by binding to this region. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (AAT09299-302) AAT09303-9. The humanised antibodies using the PCK primers AAT09303-9. The humanised antibodies using the PCK primers AAT09303-9. The humanised antibodies were useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of protein C
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Best Local Similarity 90.6%;
Matches 328; Conservative
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(first entry)

21-DEC-1995

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25-MAR-2003
21-AUG-1995
  This is the nucleotide sequence encoding the heavy chain variable region recognises the activation peptide region (AAR88106) of the heavy chain of protein C wonoclonal antibody HPC-4 which variation peptide region (AAR88106) of the heavy chain of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is converted to activated protein C (APC) by cleavage between the Arg-Leu prevents protein C activation the APC by cleavage between the Arg-Leu prevents protein C activation to APC by binding to this region. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (AAT05299-302) were used to construct humanised antibodies using the PCR primers AAT09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 417 BP; 89 A; 108 C; 106 G; 114 T; 0 other;
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                                                                                                                                                                                                                     Claim 4; Page 29-30; 41pp; English
                                                                           OKLA-) OKLAHOMA MED RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.78;
                         95WO-US07372
                                                94US-0259321
                                                                                                                                                                   Calcium-binding monoclonal
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Best Local Similarity 90.6
Matches 328; Conservative
                                                                                                   Esmon CT, Rezaie A;
                                                                                                                             WPI; 1996-049681/05
                                                                                                                                           P-PSDB; AAR88107.
                                                                                                                                                                                                                                                                                                                                                                                                            protein C to APC
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                       09-JUN-1995;
                                                  10-JUN-1994;
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AAQ75889 standard; cDNA; 418 BP

RESULT 14 AAQ75889

AAQ75889

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The sequence of the gene encoding the heavy chain variable region of the mouse anti-human interleukin-6 (IL-6) antibody. The fragment was amplified by primers (AAQ756.87) from cDNA derived from mRNA from mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19 concerned pasmid pUC-SK2-Vh. The inserted fragment is used to generate constructs (see AAQ75914-7) encoding fragments of an antibody to the human IL-6 comprising (a) a light chain with (i) a variable region containing 3 complementarity determining regions (CDN) (AAR77201-3) inserted into several framework regions (FR) (AAR77201-3) and (ii) a human light chain constant region and (b) a heavy chain with (i) a variable region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and (ii) a human light chain constant region. The FR of the light chain may be mouse derived (AAQ75888) or from the human antibody REI. The heavy chain FR may also be mouse derived (AAQ75888) or from the human antibody CDAW. The antibodies are used in the treatment of IL-6 related disorders. The antibodies are used in the treatment of IL-6 related disorders. The natived sequences and low antigenicity mouse derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 117
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                                                    Primer, PCR, amplify, kappa; light chain, variable region; mouse; human; interleukin; antibody; hybridoma; CDR; framework; constant region; heavy chain; disorder; antigenicity; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody against {\tt IL-6} - useful for the therapy and treatment of {\tt IL-6} related disorders.
                                                                                                                                                                                                /*tag= a /product= mouse heavy chain variable region 1..57 /*rag= b 58..417 /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 418;
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Mouse heavy chain variable region in plasmid pUC-SK2-Vh.
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Pred. No. 1.2e-79;
0; Mismatches 35;
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Best Local Similarity 89.5%;
Matches 325; Conservative
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(CHUS ) CHUGAI PHARM CO LTD.
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P-PSDB; AAR67655.
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                                                                                                     TATAACCCAGCCCTGAAAGGCCCGGCTCACAATCTCCAAGGATACCTCCAACAACCAGGTA
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                                                                                                                                                                       GTCTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC
                                                         178 CAGCCTTCAGGGAGGGTCTGGAGTGGCTGGCACACTTTGGTGGAATGATGATAAGTAC
                                                                                                                                                                                                                                                                                                                                                                  Anti-Streptococcus mutans surface antigen MAb SWLA2 VH coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of cariogenic organisms -
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/product=
/product= "SWLA2 heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans; monoclonal antibody; Mab; mouse; chimeric antibody; antibody; anticaries; transgenic plant; transgenic animal; caries; immunotherapy; therapy; gene; ss.
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MORRISON S L.
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P-PSDB; ABB79728.
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The present sequence is the coding sequence of the heavy chain variable region (VH) of the murine monoclonal antibody SWLAZ (19G9), which binds specifically to the surface antigens of cariogenic type c Streptococcus mutans (ATCC 25.75). The coding sequence was cotained from SWLAZ (ATCC HB 12560) hybridoma calls by PCR amplification (see also ABN84625 and ABN84622). The SWLAZ VH and VL (see ABN84608) coding sequences were used in the preparation of chimeric monoclonal antibody TEFE comprising SWLAZ variable regions and human antibodies can be used to prevent or treat dental caries in humans. The antibodies can be used to prevent or treat dental caries in humans. The antibodies can be used to prevent or treat dental caries in humans system when they bind cariogenic organisms, resulting in their destruction. The antibodies may be produced in edible plants, in transgenic animals, or in chicken eggs for oral ingestion.
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88.0%;
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CA578844 K0729C06-
BE309336 601093720
BF583109 602098016
                                                                         January 14, 2004, 15:52:50; Search time 1460.9 Seconds (without alignments) 6039.083 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                  22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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CA578844
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em_estmu:*
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Match Length DB
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gb_estl:;
gb_est2:;
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ALIGNMENTS

SULT 1	
COR	CA580198 451 bp mRNA linear BST 19-NOV-2002
SFINITION	K0748C01-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
	cDNA Library (Long) Mus musculus cDNA clone NIA: K0748C01
	IMAGE:30078168 5', mRNA sequence.
CESSION	CA580198
REION	CA580198:1 GI:25128589
SYWORDS	BST.
URCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
SPERENCE	1 (bases 1 to 451)
AUTHORS	Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
	Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
TITLE	Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
	(<u>hin-/c-Kit-/Sca-1-)</u> cDNA Library (Long)
JOURNAL	Unpublished
MMENT	Other ESTs: K0748C01-3
	Contact: Dawood B. Dudekula
	Laboratory of Genetics
	National Institute on Aging/National Institutes of Health
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
	Email: cdna@lgsun.grc.nia.nih.gov
	Plate: K0748 row: C column: 01
	Sed primer: M13 Reverse

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Pred. No. 6e-84;
0; Mismatches 17; Indels 3;
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'db_xref="taxon:10090"
'clone="NIA:K0748C01 IMAGE:30078168"
                                                                                                             organism="Mus musculus"
High quality sequence stop: 451
POLYA=No.
                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6NCr"
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Matches 346; Conservative
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Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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                                                                                                                                                               DB 10; Length 864;
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Pred. No. 6.6e-78;
0; Mismatches 19; Indels
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4218099"
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus

I (bases 1 to 864)

I (bases 1 to 864
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/note="Organ: mammary, Vector: pCMV-SPORT6, Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                                             CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
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     DB 14; Length 485;
  Score 322.8; DB 14; Length
Pred. No. 6.2e-84;
0; Mismatches 17; Indels
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'dev_stage="7 months"
lab_host="DH108"
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/strain="C57BL/6J"
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  Query Match
Best Local Similarity 94.5%;
Matches 346; Conservative
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                                                                                                                                 43 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCACTCTG 102
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amamalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (Dases 1 to 913)
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9797 row: p column: 04
High quality sequence stop: 656.
                                                                                                                                                                                                                                                                                            CTATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGT
                                                                                 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
    Gaps
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BRI78694 11-OCT-2000 MRNA linear EST 31-OCT-2000 001806679F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:4037587 5',
                      /db_xref="taxon:10090"
/clone="IMAGE:4983155"
/lab_bnost="DH10B (Ti phage-resistant)"
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/clone lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

1 186 c 159 g 164 t
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Mus musculus
Mus musculus
Musryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 940)
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighs, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM3314 row: n column: 20
High quality sequence stop: 631.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                              Query Match 82.3%; Score 298.6; DB 12; Length 666; Best Local Similarity 91.5%; Pred. No. 9e-77; Matches 343; Conservative 0; Mismatches 19; Indels 13;
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 666)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (TI phage-resistant)"
/clone_ilb="NOI GAP COST"
/clone_ilb="NOI GAP COST"
/note="Organ: colon; Vector: pGWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NOI_CGAP Library."
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation. Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMlogy row: e column: 12
High quality sequence stop: 658.
Location/Qualifiers
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BG963304 652 bp mRNA linear EST 12-JUN-2001
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                                                                                                                                                                                                                                                                                                                    /db.xcef="taxon:10090"
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/lab_nost="DH10B (TI phage-resistant)"
/lab_nost="DH10B (TI phage-resistant)"
/clone lib="WOT CGAP Co34"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.Average insert size 1.6 &b. Constructed by Life
Average insert size 1.6 &b. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                       found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov
Plate: LLMM13896 row: o column: 20
High quality sequence stop: 669.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                    musculus"
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Mus musculus
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/mol_type="mRNA"
/strain="FVB/N"
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Matches 319; Conser
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| organism="Mus musculus"
| mol_type="maxNa"
| mol_type="maxNa" | moltone | months |
| / tissue_type="tumor, gross tissue" |
| / done_tip="nonths" |
| / done_tip="nonths" |
| / done="tumor, gross tissue" |
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AGENCOURT 8836910 NCI CGAP CO24 Mus musculus cDNA clone IMAGE:6398059 5', mRNA sequence.
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Mus musculus (house mouse)

Mus musculus (bazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 947)

NHH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Pred. No. 6.8e-76;
0; Mismatches 32; Indels
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Best Local Similarity 89.7%;
Matches 331; Conservative
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K0731E07-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
cDNA Library (Long) Mus musculus cDNA clone NIA:K0731E07
IMAGE:30076566 5', mRNA sequence.
CA579006
                                                                                                                                                                                                                                                                                                                                                                                                                                              /Globellibelsoares mammary_gland_NMLMG"

/Globellibelsoares mammary_gland_NMLMG"

/Globelsoares pT773D-Pac (Pharmacia) with a modified

/Globelsoares pT773D-Pac (Pharmacia)

/Globelsoared from mammary

/Globelsoared from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-estranded CDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT773 vector. Library is normalized. Library

was constructed by Bento Scares and M. Fatima Bonaldo. "

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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information
MGI:947743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 CAGGITACTCTGAAAAGAGTCTGGCCCTGGGATATTGCAGTCCTCCCCAGACCCTCAGTCTG
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Pred. No. 8.2e-71;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                           Trace considered overall poor quality Seq primer: -40RP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                        1. 391
/organism="Mus musculus"
/nol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1531643"
/sex="female (lactating)"
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 95.0%;
Matches 287; Conservative
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291 bp mRNA linear EST 02-JUN-2000 ugd4h06.71 Soares mammary gland NNLMG Mus musculus cons clone IMAGE:1531643 5' similar to SW:HVZH HUWAN P0443B IG HEAVY CHAIN V-II REGION SESS PRECURSOR. [1]; "MRNA sequence.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Muses 1 to 391)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 CCTTATTTGCCTATTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACGTCTCC
  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.row: l column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 281.4; DB 12; Length 652;
Pred. No. 1e-71;
0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                   High quality sequence stop: 648.
Location/Qualifiers
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Matches 312; Conservative
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Gaps

115

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0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated
        TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGGAACCAGGTA
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/lab_host="DH10B"

    .485
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                      GICTCCICA 363
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/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="N1A Mouse Hematopoietic Stem Cell
/clone lib="N1A Mouse Hematopoietic Stem Cell
(Lin-/G-Kit-/Sca-l) cDNA Library (Long)"
/note="Vector: pSPORTI (Invitrogen); Site_1: Sall; Site_2:
Not!; Mouse cDNA project by the Laboratory of Genetics,
Not!; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA). Intramural Research
a long-transcript enriched cDNA library (Ref. Geneme Res.
11: 1553-158 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) priner [Invitrogen:
S'-pGACAGATTCAGARCGGAGCGCCCCTTTTTTTTTTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by tethanol-precipitation. The cDNAs were ligated
to Lone-linker Lib-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
CDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sal1 and Not1 enzymes
and cloned into Sal1/Not1 site of pSPORTI plasmid vector.
The DH10B E. coli host was transformed with the lightion
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yilan Plao (NIA)."
                    Figo, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished
Other_ESTS: K0731E07-3
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/db_xref="taxon:10090"
/clone="NIA:K0731E07 IMAGE:30076566"
/issue_type="Hematopoletic Stem Cell (Lin-/c-Kit-/Sca-1-
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                                                                                                                                                                                   Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0731 row: E column: 07
Seq primer: M13 Reverse
High quality sequence stop: 485
POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Matches 316; Conservative
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/dlone lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/G-Kit-/Sca-1-) cDNA Library (Long)"
/note="vector: pSPORT1 (Invitrogen); Site_1: Sal1; Site_2:
Not1; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Reller (National
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 bp mRNA linear EST 19-NOV-2002 KO733CL0-5N NIA Mouse Hematopoletic Stem Cell (Lin-/c-Kit-/Sca-1-) CDNA Library (Long) Mus musculus cDNA clone NIA:KO733Cl0 IMAGE:30076737 5', mRNA sequence.
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Piao, Y., Kargul, C., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/C-Kit-/Sca-1-) cDNA Library (Long)
    274
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/strain="C5/BL/6Nor"
/db_xref="niasST:kO733C10-5N"
/db_xref="tason:10090"
/clone="NIA:KO733C10 INAGE:30076737"
/closue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsuu-grc.nia.nih.gov
Plate: K0733 row. C column: 10
Seq primer: M13 Reverse
High quality sequence stop: 485
POLYA=No.
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us-09-759-112a-5.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (bases I to 379)
Akimura,T., Arakwa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,P., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                           /mol type="mmRa" | mol type="m
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74.8%; Score 271.6; DB 13; Length 920;
Best Local Similarity 85.8%; Pred. No. 8.6e-69;
Matches 314; Conservative 0; Mismatches 49; Indels 3;
                                                                                                                                              /organism="Mus musculus"
              High quality sequence stop: 640.
Location/Qualifiers
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to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-5. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sal1 and NoII enzymes and cloned into Sal1/NoII site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average missurt size is about 2.1 kb. The library was constructed by Yulan Plao (NIA)."
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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AGENCOURT 7578094 NCI CGAP Stl Mus musculus cDNA clone
IMAGE:6051673 5', mRNA sequence.
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Pred. No. 5.9e-69;
); Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 g
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85.6%;
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Best Local Similarity 85.6
Matches 316; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 428)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin./C-Kit-/Sca-1-) cDNA Library (Long)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTS: K0726H06-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0726 row: H column: 06
         cDNA Library (Long) Mus musculus cDNA clone NIA:K0726H06
IMAGE:30076121 5', mRNA sequence.
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/strain="C57BL/6NCr"
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Mus musculus
                                                                                              CA578658.1 GI:25127049
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                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
WR.:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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WR:http://genome.gsc.riken.go.jp,
WR:http://genome.gsc.riken.go.jp,
WR:http://genome.gsc.riken.go.jp,
Wrminci.Pr., Okazaki.Y., Muxamatsu.M., and Hayashizaki.Y.
Waralization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi.K., Fujiwake.S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muxamatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

*Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Flease visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/dev stage="adult"
/clone_lib="RKEN full-length enriched, adult male accessory axillary lymph node"
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Pred. No. 9.1e-68;
0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
/clone="G630034P22"
Contact: Yoghihide Hayashizaki
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'tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
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aa 42; Indels
/db_xref="niaEST:K0726H06-5N"
/db_xref="taxon:10090"
/clone="NIA:K0726H06 IMAGE:30076121"
                                             /dev_stage="Age_approx.10 weeks_old"
/lab_host="DH10B"
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1. .363 /organism="Mus musculus"

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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakazume, N., Sakazume, N., Sakazume, N., Saskai, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhaira, S., Tanamaka, T., Tomaru, H., Tagawa, Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary Sequencer. Genome Res. . . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Flease visit our web site (http://genome.gsc.riken.go.jp) for
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y., and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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BB870162 RIKEN full-length enriched, adult male accessory axillary
lymph node Mus musculus cDNA clone G630018N20 5', mRNA sequence.
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AUTHORS
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accessory axillary lymph node"
93 c 90 g 101 t
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Pred. No. 2.6e-66;
0; Mismatches 19;
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Job time : 1468.4 secs
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.5%;
Matches 274; Conservative
                                                                                                         sex="male"
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DENGTH: 483 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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US-08-483-636-3
                                                                                                                                                                                                                       January 14, 2004, 15:55:45; Search time 44 Seconds (without alignments) 3641.411 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3,
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Sequence 9,
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Sequence 9
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-561-30-60
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                    - nucleic search, using sw model
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No.
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Sequence 26, Appl Sequence 10, Appl Sequence 11, Appl	1113 1113 1113 2. A	Sequence 4, Appli Sequence 15, Appl Sequence 15, Appl	15, 15,	Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 19, Appl
3 US-08-545-809A-26 3 US-08-545-809A-10 2 US-08-483-636-11	2 US-08-483-632-11 4 US-09-702-705-1113 4 US-09-736-457-1113 4 US-09-142-974B-2	4 US-09-142-9748-4 1 US-08-488-376-15 2 US-08-634-223-15 2 US-08-634-224-15	2 US-08-634-400-15 2 US-08-635-878-15 2 US-08-770-057-15	3 US-09-335-697B-15 4 US-09-335-697B-15 4 US-09-740-002-15 1 US-08-488-376-19
546 630 423	423 646 714	1173 378 378 378	378 378 378	378 378 378 1428
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181.2 172.6 171	171 168.4 168.4 165	163.2 163.2 163.2	163.2 163.2 163.2	163.2 163.2 163.2 163.2
8 5 8 8 6 8	и и и и ч и и и	33 34 34 35	339 4 4 4 1 0	44 44 44 67 60 44 70

ALIGNMENTS

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Sequence 3, Application US/08483636
| Patent No. 5914110
| GENERAL INFORMATION:
| APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S. APPLICANT: Sylvester. Daniel R. |
| APPLICANT: Gross, Mitchell S. APPLICANT: Gross, Mitchell S. |
| APPLICANT: Gross, Mitchell S. |
| APPLICANT: Gross, Mitchell S. |
| APPLICANT: Gross, Mitchell R. |
| TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SIQUENCES: 75 |
| CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220 |
| CITY: King of Prussia |
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA

COUNTRY: USA

ZIP: 19406-039

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FILING DATE:
CLASSIFICATION NUMBER: US 08/11366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: PS0186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-509
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRAACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRAACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE
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121 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 180
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| Patent No. 5914110
| GENERAL INFORMATION:
| APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S. APPLICANT: Sylvester. Daniel R. |
| TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
| CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. BOX 1539 / UW2220
| CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.3%; Score 313.4; DB 2; Best Local Similarity 91.5%; Pred. No. 7.1e-99; Matches 332; Conservative 0; Mismatches 31;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILICATION NUMBER: 0.7-552-1994
ATTOCKNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTATION NUMBER: 95.186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-599
TELEFAX: (215) 270-599
TELEFAX: (215) 270-599
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
                                 PCT/US/94/10308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS
; LOCATION: 64..483
US-08-483-632-3
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US-08-483-636-9
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APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCES: 75
ADDRESSEE: Smithkline Beecham Corp./Corporate ADDRESSEE: Inithkline Beecham Corp./Corporate STREET: P.O. Box 1539 / UW2220
STREET: P.O. Box 1539 / UW2220
STATE: PA
COUNTRY: USA
                                                                                                                                                               Score 313.4; DB 2; Length 4. Pred. No. 7.1e-99; O; Mismatches 31; Indels
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08483632
Patent No. 5928904
                                                                                                                                                               Query Match
Best Local Similarity 91.5%;
Matches 332; Conservative .(
                                                          CDS
64..483
        MOLECULE TYPE: CDNA
                                                          ; NAME/KEY:
; LOCATION:
US-08-483-636-3
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                                                                          APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester. Daniel R.
APPLICANT: Sylvester. Daniel R.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS: 75
CORRESPONDENCE ADDRESS: ADDRESSEE: Salthkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 423;
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

CONTRY: USA

COMPUTER: 19406-0939

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.9%; Score 311.8; DB 2;
llarity 91.2%; Pred. No. 2.4e-98;
Conservative 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: US 08/117366
FILING DATE: UTS-1993
PRIOR APPLICATION UNMER: US 08/136783
APPLICATION WINBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: OT-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERNICE/DOCKET NUMBER: P50186-3
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
          Sequence 9, Application US/08483632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                     Patent No. 5928904
GENERAL INFORMATION:
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Best Local Simil
Matches 331; C
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LOCATION:
US-08-483-632-9
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Pred. No. 2.4e-98;
0; Mismatches 32; Indels 0
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                    PALLICAN NOTICE.

PARTICULAR DATE:

CLASSIFICATION: 424

PRICR APPLICATION DATA:

APPLICATION NUMBER: US 08/117366

FILING DATE: 07-5EP-1993

PRICR APPLICATION NUMBER: US 08/136783

FILING DATE: 14-OCT-1993

PROCR APPLICATION NUMBER: US 08/136783

FILING DATE: 07-5EP-1994

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-5EP-1994

ATOONEY/AGENT INFORMATION:

NAME: SULLON, Jeffrey A.

REGISTRATION NUMBER: P50186-3

TELEGOMUNICATION INFORMATION:

TELEFONE: (215) 270-5090

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 423 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOOLOGGY: unknown

MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.2%;
Matches 331; Conservative
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; LOCATION:
US-08-483-636-9
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TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA 240 241 TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCCAAGGATACCTCCAGCAACCAGGTA 300

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RESULT 4 US-08-483-632-9

Gaps

Indels

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427 ACTIGITICITICICIDEGETITICACTEAGEACTICIDEGIATEGETETEGETETEGETICET 486
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GTGAGCTGGATTCGA 120
                                                                                                                                        487 CAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACATTTATTGGGATGATGAACAC
                                                                                                                                                                                                                                                                                                                   241 ITCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAG-
                                                                                                      CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC
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LOCATION: 1.57
OCHER INFORMATION: /note= "Signal peptide encoded by
OTHER INFORMATION: nucleotides 1 through 57."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application PC/TUS9507372

Sequence 9, Application PC/TUS9507372

GENERAL INFORMATION:

APPLICANT: Oklahoma Medical Research Foundation
ITILE OF INVENTION: Calcium Binding Recombinant
ITILE OF INVENTION: Calcium Binding Recombinant
ITILE OF INVENTION: Antibody Against Protein C
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: 1200 Mest Peachtree Street
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 1201 West Peachtree Street
STREET: Atlanta
CONPITY: Becoming
CONPITY: Becoming
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEACHTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/07372
FILING DATE:
CLASSIFICATION
MEDIUM TYPE: Allanta
STORNEY AGENT INFORMATION:
MARE: PEACH INFORMATION:
MARE: PEACH INFORMATION:
MARE: PEACH INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (404) 873-873
INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727 Accercrecrea 738
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61 ACTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
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PCT-US95-07372-9
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                                                                                                                               301 GICTCTCTAACTGCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360
                                                                            301 TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACATACTACTGTGCTCGAAGA 360
                                                                                                                                                                                      361 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCC 420
                         TICCTCAAGAICACCAGIGIGGACACICGAGAIACIGCCACAIACIACIGIGCICGAAGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHIMANTRA, TOSHIRO
APPLICANT: SHIMANTRA, TOSHIRO
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: NAKAZAWA, HARUMI
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202

ZIP: 22202

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.4%; Score 299.2; DB 1;
Best Local Similarity 90.1%; Pred. No. 7.3e-94;
Matches 335; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICALLO.

PILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 028173/1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5639455man F.
RECHESTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-661-0
TELECOMMUNICATION INFORMATION:
""": FPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08197834 Patent No. 5639455 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic a DESCRIPTION: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERAX: (703) 411-2220
TELEX: 24885 OPPT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
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(: U.S.A.
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, LOCATION: 1..7
US-08-197-834-6
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58 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 TATAACCCAGCCCTGAAAGGCCGGCTCACAATCTCCAAGGATACCTCCAACAACAACCAGGTA 297
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; Patent No. 6121423
; Patent No. 6121423
; GENERAL INFORMATION:
    APPLICANT: SATO, Koh
    APPLICANT: APTO, Koh
    APPLICANT: HIRATA, Yuichi
    TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
    TITLE OF INVENTION: REPLACE
    NUMBER OF SEQUENCES: 91
    CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Foley & Lardher
    STREET: 3000 K Street, N.W., Suite 500
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 291; DB 2;
Pred. No. 3.8e-91;
0; Mismatches 35;
ATTORNEY/AGENT INPORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2020/672-5390
TELEFAX: (2020/672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE nucleic acid
TYPE nucleic acid
TYPE nucleic acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5%;
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat peptide LOCATION: 1..417
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1..417
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LOCATION:
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US-08-553-501A-28
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                                                                                                                                                                                                                                                                                   1 CAGGITACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                 58 CAGGITACICIGAAAGAGICIGGCCCIGGGAIATIGCAGCCCICCCAGACCCICACICIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACTTTACTGGGATGATGACAAGCGC
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     'n
                                                                                                                                                                               Score 296.4; DB 5; Length 417;
Pred. No. 5.1e-93;
0; Mismatches 31; Indels 3,
                                                                              /note= "Mature peptide encoded by nucleotides 58 through 417."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: STATO, Kuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLRAIN SIGNAL FOLDS/NS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSIFTCATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: Patentin Palana
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8.08-08-53-501A-28
9. Sequence 28, Application US/08553501A
9. Patent No. 5856135
                                                                                                                                                                            Query Match
Best Local Similarity 90.6%;
Matches 328; Conservative (
                     NAME/KEY: misc feature
CCATION: 58.417
OTHER INFORMATION: /not
PCT-US95-07372-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20
CLASSIFICATION:
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TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
; LOCATION: 21..449
US-08-436-463-1
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          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                      PRICOR APPLICATION:
PRICOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-129787
FILING DATE: 31-MAY-1993
ATTORNEY/AGENT INPORMATION:
NAME: WEGNER, HAROLG 25,258
REFRENCEY/DOCKET NUMBER: 53466/177/AAOK
TELEPHONE: (202)672-5399
TELEPRAN: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/YEY: mat_peptide
; LOCATION: 1..417
US-09-205-231-28
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..417
                                                                                                                                         FILING DATE:
CLASSIFICATION:
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RESULT 9

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258 TATAACCCAGCCCTGAAGAGCCGACTGACTATCTCCAAGGATACCTCCAGCAGCCAGGTA 317
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPAtible

OPERATING SYSTEM:

OFERATING SYSTEM:

OFFRAFE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,463

PILING DATE: 26-JUN 1995

CLASSIFICATION DATE: 36

PRIOR APPLICATION DATE: 37

APPLICATION NUMBER: JP 341255/1992

ATORNEY/AGENT INFORMATION:

NAME: YUN, Allen C:

REGISTRATION NUMBER: 37,971

RESTERNICE/DOCKET NUMBER: 37,971

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                            for Producing Humanized Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 441..806
OTHER INFORMATION: /product= "RAT IMMINOGLOBULIN HEAVY
OTHER INFORMATION: CHAIN VARIABLE REGION"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: CRAMPORD, Arthur R
TELEPHONE: (703)816-4100
TELEFAX: (803)816-4100
TELEFAX: (803)816-4100
TELEFAX: 200797 NIXN UR
TELEPHONE: 7031816-4100
TELEFAX: 200797 NIXN UR
TELEFAX: 100007 II:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPPOLOGY: Illnear
TOPPOLOGY: Illnear
TOPPOLOGY: Illnear
                                                                                                                                                                                                                                                                                                                                          CITY: Arlington STATE: Virginia COUNTRY: U.S.A. ZIP: 22201-414 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PSTEM: PC-DOS/MS-DOS SOFTWARE: PSTEM: Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/408,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: join(300..345, 429..806)
; OTHER INFORMATION:
US-08-408-133-1
                                                                                                                                                                                                                                                                                                  E: Nixon & Vanderhye, P.C.
No. 5750078th Glebe Road
              Sequence 1, Application US/08408133
Patent No. 5750078
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HANDI, No. 575078uo
APPLICANT: HANDI, No. 575078uo
APPLICANT: MIYAJI, Hiromasa
APPLICANT: KUMANA, Yoshihisa
TITLE OF INVENTION: Antibody
NUMBR OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: HYbridoma KM50
FEATURE:
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LOCATION: 256.7262
OTHER INFORMATION:
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LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
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US-08-408-133-1
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121 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACTTTACTGGGATGATGACAAGCGC 180
                                                                                                                                                                                                                                                                                                                               181 TATAACCCATCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA 240
                                                                                                                                                                                                                                                                                                                                                                                   621 TACAATCCATCTCTGAAAAACGGCTCACAATCTCCCAAGGACACCTCCAACAACAAGGA 680
441 CAGGTTACTCTGAAAGAATCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 500
                                                              61 ACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTCGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GICTCTCTAACTGCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCACGCTC 357
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                                                                                                                                                                                                                                                             561 CAGTCTTCAGGGAAGGGTCTGGAGTGGCTGGCAAACGTTTGGTGGAGTGATGCTAAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08454683
Sequence 1, Application US/08454683
Patent No. 5807548
PAPLICANT: BADTALA, Kenya
APPLICANT: HANAI, No. 5807548uo
APPLICANT: MIYAJI, Hiromasa
APPLICATION NUMBESS:
ADDRESSE: No. 8807548th Glebe Road
CITY: ALINGTON
STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PROCEMPATH
COMPUTER: EN PROCEMPATH
COMPUTER: EN PRECEDIATION
SOFTWARE: PARTHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: APPLICATION NUMBER: US/08/454,683
FILING DATE: AL-
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APPLICATION NUMBER: US/08/408,133
FILING DATE:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE:
ATTACK ATTACK
NAME: CRAWPORD, Archur R
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KMS0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 82.2
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: TATA signal
LOCATION: 261.267
US-08-116-778E-16
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US-08-454-680-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIGITCTITCTCTGGGGTTTTCACTGAGCACTICTGGTATGGGTGTGAGCTGGATTCGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAAGGATACCTCCAGCAACCAGGTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAATCCATCTGTGAAAACCGGCTCACAATCTCCAAGGACACCTCCAACAACAAGCA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTCAAGATCACCAATATGGACACTGCAGATACTGCCATATACTACTGTGCTGGGAGA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GICTCTCTAACTGCCTATGCTA - - TGGACTACTGGGGTCAAGGAACCTCAGTCACGTC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGCTACGGAGGGTATAGTGAGCTTTGATTACTGGGGCCACGGAGTCATGGTCACAGTC 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGGITACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.1%; Score 250.8; DB 1; Length 812; Best Local Similarity 82.2%; Pred. No. 4.6e-77; Matches 301; Conservative 0; Mismatches 62; Indels 3
                                                                                                                                                                                                                                                                                                                       /product= "RAT IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION"
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Sequence 16, Application US/08116776E

Patent No. 5830470

GENERAL INFORMATION:
APPLICANT: NAKAMIRA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOSUO
APPLICANT: HANAI, NOSUO
APPLICANT: HASEGRAWA, MAMORU
ITTLE OF INVENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                         FEATURE:
LOCATION: 256.762
COTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 441.806
OTHER INFORMATION: CHAIN VARIABLE REC
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 300.440
OTHER INFORMATION:
FEATURE:
NAME/KEY: Sig_peptide
LOCATION: 300.440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300.345, 429.806)
                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: Hybridoma KM50
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local
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Pred. No. 4.6e-77;
0; Mismatches 62; Indels 3
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER EXADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION NUMBER: 249-59
REFERENCE/POCKET NUMBER: 32,955
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240 680

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                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22201
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRAFING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATEMILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
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Pred. No. 4.6e-77;
0; Mismatches 62;
                                                                                                                                                                                                                                         ALUKESEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION NUMBER: JP 3-238375
FILING DATE: 18-SEP-1991
ATTONNEY AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 249-74
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
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Sequence 1, Application US/08454680
                                       GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHHIISA
TITLE OF INVENTION: PROCESS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.2%;
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide.
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STRANDEDNESS: double
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-454-680-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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1 CAGGITACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 60

Gaps

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62; Indels

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61 ACTIGITCITICICIGGGITTITCACTGAGCACTTCTGGIAIGGGIGTGAGCTGGATTCGA 120
                                                                                                                                                                              CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACTTTACTGGGATGATGACAAGCGC 180
                                                                                                                                                                                                                                   s61 cagrerreagggaagggrerggagregeergeeaaacgrrregregagreargargeraagrae 620
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441 CAGGTTACTCTGAAAGAATCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 500
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                                                                                                                   CITY: ARLINGTON
STATE: LICO NORTH GLEBE NOAD
CONTRX: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FOCDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CLEASIFICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLEASIFICATION: 424
FRING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILLSON, MARY J.
RESERRENCE/DOCKET NUMBER: 249-76
TELESCOMMUNICATION NUMBER: 249-76
TELESCOMMUNICATION NUMBER: 249-76
TELESCOMMUNICATION NUMBER: 249-76
TELESCOMMUNICATION NUMBER: 249-76
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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HOSEGUENCES: 49
CORRESPONDENCES: 49
CORRESPONDENCE ADDRESSS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16, Application US/08438562
; Patent No. 5874255
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR
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                                                                                                                                                                                                                                                              441 CAGGTTACTCTGAAAGAATCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 500
                                                                                                                                                                                                                                                                                                    ACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTCGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCTCAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGAAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 TTCCTCAAGATCACCAATATGGACACTGCAGATACTGCCATATACTACTGTGCTGGGAGA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTCTCTAACTGCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCACGTC 357
                                                                                                                                                                                                                                                                                                                                                                                                                CAGTCTTCAGGGAAGGGTCTGGAGTGGCTGGCAAACGTTTGGTGGAGGAATGCTAAGTAC
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      3;
                                                                                                                                                  Length 812;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-UUN-95
                                                                                                                                                    DB 2;
                                                                                                                                                                      4.66-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NATAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                  Score 250.8;
Pred. No. 4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08483528B Patent No. 5939532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
                                                                                                                                                                                                                            1 CAGGTTACTCTGAAAGAGTC
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                  69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIF: 22201-4714
COMPUTER READABLE FORM:
                                STRAIN: HYBRIDOMA KM50 FEATURE:
                                                                                                                                                Query Match
Best Local Similarity 82.2
Matches 301; Conservative
                                                                        NAME/KEY: TATA signal
LOCATION: 261.7267
US-08-438-562-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 TCCTCA 363
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STREET: 11
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                                                                                                                                                                                                                                                                                                                    Length 812;
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                                                                                                                                                                                                                                                                                                                 Score 250.8; DB 2;
Pred. No. 4.6e-77;
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                     STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                 69.1%;
  16:
                                                  : 812 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                              STRAIN: HYBRIDOMA KM50
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.2
Matches 301; Conservative
SEQ ID NO:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                         ) NAME/KEY: TATA signal
; LOCATION: 261..267
US-08-483-528B-16
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FEATURE:
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Sequence 11, Appl
Sequence 7, Appli
Sequence 4, Appli
Sequence 1, Appli
                                                      January 14, 2004, 16:03:20 ; Search time 215.81 Seconds (without alignments) 5928.789 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1, Ap
Sequence 50, A
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Sequence 3,
Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5,
                                                                                                                     1 caggttactctgaaagagtc......sctcagtcaccgtctcctca 363
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(c) 1993 - 2004 Compugen Ltd.
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0 US-09-759-112A-6
0 US-09-879-461-3
0 US-09-879-461-9
3 US-10-010-942B-15
1 US-09-559-11
US-09-81-823-7
2 US-10-323-903-4
US-09-764-304-1
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                      2324096 segs, 1762381658 residues
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Maximum Match 100%
Listing first 45 summaries
                                     OM nucleic - nucleic search, using sw model
                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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363
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Match Length
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Perfect score:
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Sequence 22, Appl		N	m	N	σ	H	9	٦	4	Ä	œ	equence 2	Ň	Ň	equence 1	H	H	H	H	H	4	Sequence 2, Appli	4	15	-	5	-0	N	Sequence 1, Appli
10-071-866-2	10-071-866	10-360-828-2	10-360-828-3	10-108-260	10-225-108A-	-995-5	09-972-656-6	-10-072-301-1	-998-	-10 - 360 - 828 - 1	-959-	-301-2	-866-	-828-	-09-879-4	-09-736-45	09-902-941-111	-626-111	72-11	-10-017-754-111	-940-544	US-10-075-947A-2	10-075-94	9-740-002-1	US-10-384-356-15	9-740-002-1	10-38	-93	US-09-797-941A-1
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183	183	183	183	182.6	180.4	179.2	178.6	173.4	173.4	173.4	172	171.8	171.8	171.8	171	168.4	168.4	168.4	168.4	œ,	φ	ø	9	m.	63.	m.	63.	162	•
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ALIGNMENTS

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Sequence 5, Application US/09759112A

Sequence 5, Application US/09759112A

Publication No. US20030100741A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WIGLECTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHTITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE TITLE OF INVENTION: ANTIBODIES
TITLE REFERENCE: 200-013
CURRENT PELING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0

SEQ ID NO 5
LENGHA: 363
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100.0%; Pred. No. 1.5e-114;
iive 0; Mismatches 0;
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CTHER INFORMATION: 1F7 VH chain gene US-09-759-112A-5
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Best Local Similarity 100.
Matches 363; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: mouse
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     US-09-759-112A-5
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.3%; Score 313.4; DB 10; 91.5%; Pred. No. 2e-97;
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FILING DATE: 12-Unr-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/12,929
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/136,783
ATTORNEY/AGENT INFORMATION:
NAME: SULFON, Jeffrey A.
REFERENCE/DOCKET NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.5
Matches 332; Conservative
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         361 TCA 363
                                                                                           361 TCA 363
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TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
TITLE REPERBENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT PILING DATE: 2001-01-1
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 6
LENGTH: 363
TYPE: NAV.
                                                                                                                                                 240
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; LOCATION: (1)..(363)
; COTHER INFORMATION: 1F7 VH chain gene
US-09-759-112A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09759112A Publication No. US20030100741A1 GENERAL INFORMATION:
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Sequence 7, Application US/09881823

Sequence 7, Application US/09881823

Patent No. US20020068066A1

GENERAL INFORMATION:

APPLICANT: SHI, WENYUAN

APPLICANT: ANDERSON, MAXWELL

APPLICANT: MINS, LETITIA

APPLICANT: WINS, LOSSI-032

CURRENT PILION NUMBER: US/09/881,823

CURRENT FILING DATE: 1999-08-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 7

TENDANT: APPLICANT: APPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.3%; Score 284.4; DB 9; Length 465;
88.0%; Pred. No. 1.9e-87;
Live 0; Mismatches 41; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.0
Matches 322; Conservative
   361 GTCTCCTCA 369
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; LOCATION: (13)..(441)
US-09-881-823-7
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178 CAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGGGC 237
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Best Local Similarity 90.2%; Pred. No. 1.7e-92;
Matches 333; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08995529
Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
ITILE OF INVENTION: Humanized Collagen Antibodies and
ITILE OF INVENTION: Related Methods
FILLE REFERENCE: P.IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FRAELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 Grerectes 426
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; LOCATION: (1)...(369)
US-09-995-529-11
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Pred. No. 8.8e-76;
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Publication No. US20030166876A1
GENERAL INFORMATION:
                     EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1
                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.2%;
Matches 301; Conservative
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sig_peptide
(300).. (440)
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N: (300)..(806)
Y: intron
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US-09-764-304-1
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LOCATION: (
NAME/KEY: 8
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              APPLICANT: FOSTER, SIMON
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL POSITIVE BACTERIA
FILE REPERENCE: 07787.0059
CURRENT APPLICATION NUMBER: US/10/323,903
CURRENT PILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/097,055
PRIOR FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 4
LENGTH: 357
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| Sequence 1, Application US/09764304
| Patent No. US20020026036A1
| GENERAL INPORMATION:
| APPLICANT: HANAI, NOBUO
| APPLICANT: HANAI, NOBUO
| APPLICANT: HANAI, NOBUO
| APPLICANT: KUWANA, YOSHIHISA
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
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| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| TITLE OF INVENTION: DOJUE: 1999-01-05
| EARLIER PILING DATE: 1995-03-21
| EARLIER PILING DATE: 1995-03-21
| EARLIER PILING DATE: 1994-08-17
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Pred. No. 8.5e-83;
KOKAI-KUN, JOHN FITZGERALD
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 94.3%;
Matches 281; Conservative
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LOCATION: (1)..(357)
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61 ACTIGITCITICICIGGGITTICACIGAGCACTICIGGIAIGGGIGIGAGCTGGAITCGA 120
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FEATURE:
OTHER INFORMATION: Description of Artificial Seguence: Rat Hybridoma
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APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
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SHITARA, KENYA
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Best Local Similarity 82.2%;
Matches 301; Conservative
                                                                                                                                          HANAI, NOBUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680
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                                                                                                                                                                                                                                                                                                                                EATURE:
THER INFORMATION: Description of Artificial Sequence: Rat Hybridoma
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 812;
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Pred. No. 8.8e-76;
0; Mismatches 62; Indels
PRIOR APPLICATION NUMBER: US 09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR PILING DATE: 1995-05-31
PRIOR PLING DATE: 1995-05-31
PRIOR PLING DATE: 1995-05-17
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1992-09-17
PRIOR PLING DATE: 1992-09-17
PRIOR PLING DATE: 1992-09-17
PRIOR PLING DATE: 1991-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.2%;
Matches 301; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
LENGTH: 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
(429)..(806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
(300)..(344)
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; LOCATION: (346)..(428)
US-10-166-626-1
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: TATA signal
LOCATION: (256)..(262)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
(300)..(440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: (300)..(806)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IMP POPUTED COMPUTER: IMP POPUTED COMPUTER: IMP POPUTED COMPUTER: POPUTED CONTROL OF CONT
                                                                                                                                                                                                                                                                                                                                           KUWANA, YOSHIHISA
HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/393,385B
FILLING DATE: 27-JUN-96
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: TATA signal
; LOCATION: 261..267
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-195-752-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 16, Application US/10195752
Publication No. US20030077276A1
                                                                                                 GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: HYBRIDOMA KM50
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TYPE: nucleic acid
STRANDEDNESS: double
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181
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681 TICCICAAGAICACCAATAIGGACACIGCAGAIACIGCCAIAIACIACIGIGCIGGGAGA 740
                                                 GTCTCTCTAACTGCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC 357
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHILAN, AGAINS
APPLICANT: HANNI, NOBUC
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAMA, MAMORU
APPLICANT: HASEGAMA, MAMORU
APPLICANT: MINALI, HIROMASA
APPLICANT: MINALI, HIROMASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REPREBRICE: 249-101
CURRENT FILING DATE: 2002-10-08
PRIOR PELICATION NUMBER: US/09/225,322
PRIOR PELICATION NUMBER: US/09/225,322
PRIOR APPLICATION NUMBER: US 08/464,680
PRIOR PELING DATE: 1995-01-05
PRIOR PELING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR PELING DATE: 1995-03-17
PRIOR PELING DATE: 1995-09-17
PRIOR PELING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SECTIVALE: PALCATION NUMBER: US 3-238375
NUMBER OF SEQ ID NOS: 19
SECTIVALE: PALCATION NUMBER: US 3-238375
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 1
LENGTH: 812
TWOR: NUMBER: PALCATION NUMBER: US 3-238375
TWOR: NUMBER: PALCATION NUMBER: US 3-238375
NUMBER OF SEQ ID NOS: 19
LENGTH: 812
TWOR: NUMBER: PALCATION NUMBER: US 3-238375
NUMBER OF SEQ ID NOS: 19
                                                                                           741 GGGCTACGGAGGGTATAGTGAGCTTTGATTACTGGGCCACGAGTCATGGTCACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
DTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 812;
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Pred. No. 8.8
                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.2%;
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (300)..(344)
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LOCATION: (429)..(806)
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LOCATION: (256)..(262)
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; LOCATION: (346)..(428)
US-10-265-713-1
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LOCATION: (300)..(440
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LOCATION: (300)..(806)
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441 CAGGITACTCTGAAAGAATCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG 500

62; Indels

0; Mismatches

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APPLICANT: Mezes, Peter S.
APPLICANT: Mezes, Peter S.
APPLICANT: Achard, Ruth A.
APPLICANT: Schlow, Jeffrey
APPLICANT: Conhom, Jeffrey
APPLICANT: Schlow, Jeffrey
APPLICANT: Schlow, Jeffrey
APPLICANT: Schlow, Jeffrey
APPLICANT: Schlow, Jeffrey
APPLICANT: Padlan, Eduardo A.
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
TITLE OF INVENTION: Capable of Binding to TAG-72
TITLE OF INVENTION UNMERR: US (08/961,309)
PRIOR FILING DATE: 1997-10-30
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1992-10-20
PRIOR FILING DATE: 1990-07-17
NUMBER OF SEQ ID NOS: 78
SEGFWARE: Microsoft Word 97 SR-2
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OTHER INFORMATION: DNA encoding the heavy chain variable region of the anti-N-OTHER INFORMATION: acetylglucosamine antibody, B17X2
US-10-255-478-50
                                                                                                                                                                                                                                                                                              561 cádrorroadgaadgatorgaagrocorddoaacarragagaardaargardcoraagaac 620
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501 Actriscretrictics description of the second of the sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: B17X2 VH coding sequence
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LENGTH: 423
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APPLICANT: Hua, Shao-bing
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling Michelle H.
APPLICANT: Zhu, in
APPLICANT: Zhu, in
APPLICANT: Zhu, in
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNOBER
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 25636-718
CURRENT APPLICATION NUMBER: US/10/072,301
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTMARE: Patentin version 3.1
SSOFTMARE: Patentin version 3.1
SEQ ID NOS 30
LENGTH: 759
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; OTHER INFORMATION: Clone 15.150.24 Variant
US-10-072-301-30
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                                        Sequence 30, Application US/10072301 Publication No. US20030152913A1
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ORGANISM: Artificial Sequence
JS-10-072-301-30
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CURRENT APPLICATION NUMBER: US/10/072,301
CURRENT APPLICATION NUMBER: 2002-02-08
SUNDBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VARION 3.1
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Pred. No. 1.9e-52;
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Publication No. US20030152913A1
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
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Best Local Similarity 76.3%;
Matches 225; Conservative
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January 14, 2004, 17:47:02; Search time 37.1905 Seconds (without alignments) 516.420 Million cell updates/sec
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Murine Mab 1F7 hea Mouse Mab 3B9 heav Heavy chain variab Heavy chain sequen Chimeric antibody Heavy chain variab Chimeric 3B9 monoc Il-6 binding inhib Mouse 10D5 VH prot

AAR70190 AAY23768 AAY18121

AAR70191 AAY23769 AAY18125 AAR58612 ABG76934

sed MA anti-	Murine anti-Protei	`	0 0	8	Q	ntibody	#2	۲. د	Amino acid sequenc	Anti-Streptococcus	Sequence of mouse	zed an	Heavy chain variab	chain	chain	chain s	sed 10D5	ed 10D5	Humanised 10D5 ant	Humanised 10D5 ant	Rat immunoglobulin	KM50 cell-derived	KM50 Rat immunogl	Rat activated immu		Mouse anti-RSV ant	Human RSV antibody	н	g	Ę	-RSV	Anti-RSV antibody	Anti-RSV antibody
AAR54101 AAR88109	AAR88107 AAB6766	o co		AAB09778	AAB70885	AAB21367	AAU77289	AAR92089	ABG31433	ABB79728	AAR54092	AAR70192	AAY23770	AAY18117	AAY23780	AAY18122	ABP58285	28	ABP58289	ABP58283	AAR33255	AAR53339	AAY28367	AAB01626	AAE10476	AAG63243	ABP66562	ABU69425	ABG31432	AAR92088	AAG63259	AAG63261	AAG63265
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ALIGNMENTS

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Mouse, 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.
                    AAO18528 standard; Protein; 121 AA.
                                                                                                                                                                                             11-JAN-2002; 2002WO-US00927.
                                                                                                                                                                                                               11-JAN-2001; 2001US-0759112.
                                                                            Murine Mab 1F7 heavy chain.
                                                         (first entry)
                                                                                                                                                                                                                                 (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                     Muller S, Kohler H;
                                                                                                                                                                                                                                                                       WPI; 2002-590668/63.
N-PSDB; AAL48652.
                                                                                                                                                       WO200255668-A2.
                                                         11-OCT-2002
                                                                                                                                                                          18-JUL-2002.
                                      AA018528;
                                                                                                                                     Mus sp.
RESULT 1
AAO18528
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New polynucleotide encoding a complementarity- or framework-determining

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WPI; 1999-429500/36.
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                                                                                                                                                                                            Query Match
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                                                       The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 heavy chain.
                                                                                                                                                                                                                           61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
                                                                                                                                                                                                              YNPSLKSRLTISKDISSNQVFLKIISVDIRDIATYYCARRVSLIAYAMDYWGQGISVTVS 120
                                                                                                                                                                         9
                                                                                                                                                                                           1 QVILKESGPGILQPSQILSLICSFSGFSLSISGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
                                                                                                                                                                         1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV
                                                                                                                                                       ö
                                                                                                                                  100.0%; Score 633; DB 23; Length 121; 100.0%; Pred. No. 7.3e-55; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "complementarity determining region"
11..86
|abel= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "complementarity determining
                                      Disclosure; Page 18-19; 27pp; English.
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    AAR70190 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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/label= CDR
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93US-0136783
                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Mouse MAb 3B9 heavy chain.
                                                                                                                                            Best Local Similarity 100.
Matches 121, Conservative
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label= '
                                                                                                                 121 AA;
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14-OCT-1993;
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20-SEP-1995
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Peptide
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61 YNPSLKSRLTISKDISSNQVFLKIISVDIRDIATYYCARRVSLTAYAMDYWGQGISVTVS 120
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                                                                                                                                                                                                                                                       Spleen cells from mice immunized with human IL-4 were used to prepare hybridomap, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGEN/F+ and transformed into B. coli DHS-alpha. The clones were sequenced (AAQ83490-91), and used for antibody engineering.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVTLXESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                 Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 140;
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Pred. No. 1.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes SD, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY23768 standard; Protein; 140 AA.
                                                                                                                                                                                                        Disclosure; Fig.2; 97pp; English.
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93US-0117366.
93US-0136783.
94WO-US10308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.1
Matches 109; Conservative
WPI; 1995-123387/16.
N-PSDB; AAQ83491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 140 AA;
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07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease, allargic disorder, allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy, autoimmune disease; graft versus host disease.
                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                          79
                                                                         The present sequence represents the heavy chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Inmunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermaltis, atopic asthma, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease, rhey are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
                                                                                                                                                                                                                                                                                                          20 OVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                    1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                               Gaps
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0
                    New DNA molecules encoding recombinant antibodies useful for treating IL4-mediated conditions
                                                                                                                                                                                                                                        Length 140;
                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                       Score 569; DB 20;
Pred. No. 1.8e-48;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain sequence for murine 3B9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gross MS, Holmes SD, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18121 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                      Example 3; Fig 2; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0483636.
93US-0117366.
93US-0136783.
                                                                                                                                                                                                                                       89.9%;
90.1%;
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.1
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-370482/31.
N-PSDB; AAX79520.
                                                                                                                                                                                                                 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  140 S 140
                                                                                                                                                                                                                                                                                                                                                                             121 S 121
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07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1995;
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                                                                                                                                                                                                                   Sequence
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80 YNDSLKSRLTISKDISSNQVFLKITSVDIADIATYYCARRETVFYWYFDVWGAGTTVTVS 139
                                                                             This sequence represents the heavy chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (II4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, aropic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
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                                                                                                                                                                                                                                                                                                                                                           Score 569; DB 20; Length 140;
Pred. No. 1.8e-48;
4; Mismatches 8; Indels (
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/label= CDR
/note= "complementarity determining region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..19
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70191 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibody 3B9 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAb; interleukin-4; IL-4; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
                                           Claim 24; Fig 2; 50pp; English.
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90.18;
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93US-0136783.
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/label= CDR
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|abel= CDR
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(first entry)
Recombinant IL4 antibodies
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.1
nes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens; Mus sp
                                                                                                                                                                                                                                                                                                                    140 AA;
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14-OCT-1993;
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20-SEP-1995
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                                                                                                                                                                                                                                                                                                                    Sequence
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region of

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murine/human interleukin-4 (idea) chimeric antibody 389. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic thinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheny are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. b) ELISA of circulating endogenous IL-4 levels in humans.
                                                                                        New DNA molecules encoding recombinant antibodies useful for
                                                                                                                                                                                    The present sequence represents the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes SD, Sylvester DR;
 Sylvester DR;
                                                                                                               treating IL4-mediated conditions
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                                                                                                                                                 Example 3; Fig 3; 50pp; English
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93US-0117366.
93US-0136783.
94WO-US10308.
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Matches 109; Conservative
 Holmes SD,
                                     WPI; 1999-429500/36.
                                                        N-PSDB; AAX85886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 S 121
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14-OCT-1993;
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Gross MS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region, interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction; Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                       A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human IL-4 MAB 3B9 variable region including 3 CDRs (AAR70198-200) and a human antibody signal peptide (AAR70193). The construct was used (for humanized antibody production.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                             Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated and IgE-mediated allergic conditions
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

89.9%; Score 569; DB 16; Length 141;
Best Local Similarity 90.1%; Pred. No. 1.8e-48;
Matches 109; Conservative 4; Mismatches 8; Indels C
                                       Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY23769 standard; Protein; 141 AA
                                                                                                                                                                                                       Disclosure, Fig. 3; 97pp; English
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 (SMIK ) SMITHKLINE BEECHAM PLC
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93US-0117366.
93US-0136783.
94WO-US10308.
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Chimeric - Homo sapiens.
                                       Holmes SD,
                                                                        WPI; 1995-123387/16.
N-PSDB; AAQ83492.
                                                                                                                                                                                                                                                                                                                                                                            141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S 141
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07-SEP-1994;
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                                         Gross MS,
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AAY23769
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81 YNPSLKSRLTISKDISSNOVFLKIISVDIADIATYYCARRETVFYWYPDVWGAGTIVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody, interleukin-4, IL4, immunoglobulin E; IgE mediated disease; allergic disorder, allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autoimmune disease; graft versus host disease.
                                                                                                                                                         09
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                                                                                                                                                         1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                              21 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                           61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS
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89.9%; Score 569; DB 20; Length 141; 90.1%; Pred. No. 1.8e-48; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric 3B9 monoclonal antibody heavy chain.
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Gaps

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Polypeptide inhibiting binding of human interleukin-6 (IL-6) to its receptor - useful for treating auto:immune disease induced or aggravated by IL-6
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                       Recombinant IL4 antibodies
                                                                                                                                       Matches 109; Conservative
                                                                                                                                                                                                                                                                                                Il-6 binding inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                            Hamuro J, Nakazawa H,
                                                                                                                                                                                                                                                                                                                                                                                               (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-295777/37.
N-PSDB; AAQ70612.
     WPI; 1999-370482/31.
N-PSDB; AAX79542.
                                                                                                                                  Similarity
                                                                                                                                                                                                        121 $ 121
                                                                                                                                                                                                                    141 S 141
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                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                             25-MAR-2003
28-APR-1995
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                 AAR58612;
                                                                                                                            Query Match
Best Local
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183 YNPSLKSRLTISKDTSTNQVFLKITSVDTADTATYFCARR-SLYGNWGDYAMDYWGQGTS 241
                                                                                                                                                                                                                                                                                                                                  123 QVKLEESGPGILQPSQTLSLTCSPSGPSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKH 182
                                                                                                                                                                                                                                                                                                                                                                          YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTA----YAMDYWGQGTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; humanized, immunoglobulin, Ig, light chain, LC; heavy chain; HC; variable region complementarity determining region, 3D6; 10D5; variable framework region, amyloidogenic disease; Alzheiner's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
                                                                                                                                                                                                                                                                                               QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor immunoglobulin
                AAQ70612 codes for human interleukin-6 binding inhibitor, the polypeptide disesribed in AARS6612. This polypeptide lihibite the binding of human II-6 to its receptor, and can therefore be useful in the treatment of a variety of autoimmune diseases; specifically in the treatment of rheumatoid architis, septic shock due to bacterial infection and multiple myeloma. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                Score 567.5; DB 15; Length 246; Pred. No. 4.9e-48; 3; Mismatches 5; Indels 5;
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                                                                                                                                                                                                                Query Match
Best Local Similarity 89.6%;
Matches 112; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse 10D5 VH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basi G, Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEUR-) NEURALAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-519658/55.
N-PSDB; ABS59429.
                                                                                                                                                                            246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTVSS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200246237-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG76934;
                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abeta.
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ABG76934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 YNPSLKSRLTISKDTSSNQVFLKITSVDTADTATYYCARRETVFYWFDVWGAGTTVTVS 140
                                                                                                                                             This sequence represents the light chain of the chimeric 3B9 antibody of the invention. The antibody is a chimeric or Munanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ÓVTLKESGPGILÓPSÓTLSLTCSFSGFSLSTSGMGVSWIROPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVTLKESGPG1LQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAH1YWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                            Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                        Score 569; DB 20;
Pred. No. 1.8e-48;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARS8612 standard; Protein; 246 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        septic shock; multiple myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimamura
                                                                                                              Example 5; Fig 3; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                        89.9%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94EP-0102346
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(first entry)
                                                                                                                                                                                                                                                                                                                                                     141 AA;
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The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/10D5 Ig LC or HC variable region sequence,

Claim 142; Figure 10; 171pp; English.

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21-DEC-1995.
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                                                  Sequence
                                                                       Query Match
                                                                                                                                                                                                                                              RESULT 11
AAR88109
  8888888
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                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                            8
and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic disease or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present amino acid sequence represents a mouse 3D6/10D5 variable light (VL) chain or variable heavy (VH) chain protein of the invention.
                                                                                                                                                                                         80 YNPSLKSRLTISKDISKOVFLKIISVDPADTATYYCVRRPITPVLVDAMDYMGOGISVT 139
                                                                                                                                                                         61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARR--VSLTAYAMDYWGQGTSVT 118
                                                                                                                                  9
                                                                                                                                                 QATLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chains
                                                                                                                                  1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR54101-02 represent the heavy and light chain respectively of the humanised monoclonal antibody (MAD) of the invention. The antibody has the ability to neutralise human immunodeficiency virus. The antibody is classified as IgG kappa and
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                  murine; heavy; light; chain; monoclonal; antibody;
ty determining region; CDR; IgG; kappa; IIIB; IIIMN.
                                                                                                             2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant anti-HIV monoclonal antibody - capable of neutralising strains which can not be neutralised by anti-IIIB and IIIMN antibodies
                                                                                        Length 142;
                                                                                                             12; Indels
                                                                                         Score 551; DB 23;
Pred. No. 1.1e-46;
l; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                               complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAR54101 standard; Protein; 122 AA.
                                                                                                            1;
                                                                                          87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              52..67
/label= CDR2
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/label= CDR1
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92JP-0322476
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                        Query Match
Best Local Similarity 87.83
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   - Mus musculus.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                 Humanised MAb H-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-205040/25.
                                                                       142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ68709.
                                                                                                                                                                                                                 VSS 121
                                                                                                                                                                                                                                    140 VSS 142
                                                                                                                                                                                                                                                                                                                                                                    Human; mouse;
                                                                                                                                                                                                                                                                                                                           08-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP06141885-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
Chimeric
                                                                       Sequence
                                                                                                                                                    20
                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                         AAR54101;
                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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This is the amino acid sequence of the mature peptide from the murine anti-protein C monoclonal antibody HPC-4 heavy chain variable region. HPC-4 recognises the activation peptide region (AAR88106) of the heavy chain of protein C, a vitamin K-dependent plasma protein zymogen. Protein C is converted to activated protein C (APC) by cleavage between HPC-4 prevents protein C activation peptide sequence. HPC-4 prevents protein C activation the activation peptide sequence. The DNA sequences encoding the variable regions of the heavy and light chains of the antibody (AAT09229-302) were used to construct humanised antibodies using the PCR primers AAT09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNPSLKSRLTISBDTSNNQVFLKITTVDTADTATYYCARRVFYGNSDFMDHWGQGTSVTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTFGMGVSWIRQPSGKVLEWLAHIYWDDDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSL-TAYAMDYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium-binding monoclonal antibody immunoreactive with Protein C inhibits Protein C anticoagulant activation by thrombomodulin, e.g. for treating tumours
has the sequence RIGPGR or RVGPGR in the principal neutralising domain. The antibody may be used to neutralise the clinically separate strains which cannot be neitralised by the neutralising antibodies against IIIB and IIIMN strains.
                                                                                                                                                                                                                                                                                                                                       ٠<u>.</u>
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                                                                                                                                                                                                                                                                   DB 15; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.
                                                                                                                                                                                                                                                               86.3%; Score 546.5; DB 15;
87.7%; Pred. No. 2.5e-46;
ive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88109 standard; peptide; 120 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OKLA-) OKLAHOMA MED RES FOUND.
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                                                                                                                                                                                                                                                                                                       Best Local Similarity 87.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rezaie A;
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                                                                                                                                                                                           122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09534652-A1
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the PCR primers AAT09303-9. The humanised antibodies are useful as inhibitors of coagulation and can be used for the treatment of tumours by inhibiting the anticoagulant activity of APC by preventing conversion of
                                                                                                                                         82.5%; Sco...
84.3%; Pred. No. e...
... 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..19
/label= signal peptide
20..139
/label= mature peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR67655 standard; Protein; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 49; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirata Y, Sato K, Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI SEIYAKU KK.
(CHUS ) CHUGAI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP00859
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(first entry)
                                                                                                                                                   Query Match
Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody against IL-6 - IL-6 related disorders.
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                                                                                                              139 AA;
                                                                    protein C to APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ75889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1993;
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21-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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    8888888
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                                                                                                                                                                                                                                                          61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                          61 YNPVLKSRLIISKDTSRKQVFLKIASVDTADTATYYCVRMMD-DYDAMDYWGQGTSVTVS 119
                                                                                                                                                                            9
                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epitope, activation, heavy chain, protein C, vitamin K, plasma protein, zymogen, cleavage, mouse, humanised antibody, variable region, light chain, inhibition, anticoagulant, coagulation, tumour.
                                                                                                                                                                                                1 QVTLKESGPGILQPSQTLTLTCSLSGFSLRTSGWGVGWIRQPSGKGLEWLAHIWWDDDKR
                                                                                                                                                                          1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium-binding monoclonal antibody immunoreactive with Protein C inhibits Protein C anticoagulant activation by thrombin-thrombomodulin, e.g. for treating tumours
                                                                                                                                1;
                                                                                       Length 120;
                                                                                                                                15; Indels
                                                                                     DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine anti-Protein C MAb HPC-4 VH gamma protein.
                                                                                     Query Match
82.5%; Score 522.5; DB 1'
Best Local Similarity 84.3%; Pred, No. 5.8e-44;
Matches 102; Conservative 3; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR88107 standard; Protein; 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OKLA-) OKLAHOMA MED RES FOUND.
conversion of protein C to APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US07372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-049681/05.
N-PSDB; AAT09299.
                                             120 AA;
                                                                                                                                                                                                                                                                                                                                                 $ 121
                                                                                                                                                                                                                                                                                                                                                                                           120 S 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                 121
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                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
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AAR88107

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61 YNPSLKSRLTISKDISSNQVFLKITSVDIRDIATYYCARRVSLIAYAMDYWGQGISVIVS 120
                                                                                                                                  YNPVLKSRLIISKDTSRKQVFLKIASVDTADTATYYCVRMMD-DYDAMDYWGQGTSVTVS 138
                                                            9
                                                                          20 QVILKESGPGILLQPSQTLTLTCSLSGFSLRTSGWGVGWIRQPSGKGLEWLAHIWWDDDKR 79
                                                                                                                                                                                                                                                                                                                                                                                                      Primer, PCR, amplify, kappa, light chain, variable region, mouse, human, interleukin, antibody, hybridoma, CDR, framework, constant region, heavy chain, disorder, antigenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The deduced amino acid sequence of the heavy chain variable region of the mouse anti-human interleukin-6 (IL-6) antibody. The gene was amplified by primers (AAQ75876-87) from cDNA derived from mRNA from mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19 to produce plasmid pUC-SK2-Vh. The inserted fragment is used to
                                                         1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                              Gaps
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Score 522.5; DB 17; Length 139;
Pred. No. 6.9e-44;
3; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - useful for the therapy and treatment
                                                                                                                                                                                                                                                                                                                                                                            Mouse heavy chain variable region amino acid sequence.
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3
generate constructs (see AAQ75914-7) encoding fragments of an antibody to the human IL-6 comprising (a) a light chain with (i) a variable region containing 3 complementarity determining regions (CDR) (AAR77201-3) inserted into several framework regions (FR) (AAR77204-7) and (ii) a human light chain constant region and (b) a heavy chain with (i) a variable region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and (ii) a human light chain constant region. The FR of the light chain may be mouse derived (AAQ75889) or from the human antibody REI. The heavy chain FR may also be mouse derived (AAQ75889) or from the human antibody chain antibodies can be used in the treatment of IL-6 relamed
                                                                                                                                                                                   disorders. The antibodies are useful as they have low antigenicity due to the use of human derived sequences and low antigenicity mouse derived
                                                                                                                                                                                                                                                                                                                                                                                           1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
                                                                                                                                                                                                                                                                                                                                                                                                              61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAY--AMDYWGQGTSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 YNPALKGRLTISKDTSNNQVFLKIASVVTADTATYYCAR---MEDYDEAMDYWGQGTSVT
                                                                                                                                                                                                                                                                                                                                                      5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T lymphocytes and/or cytotoxic T lymphocytes able to bind to the hypervariable 1 region of the infecting HCV strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a hepatitis C virus (HCV) vaccine comprising different groups of peptides each group being capable of
                                                                                                                                                                                                                                                                                                                Score 521.5; DB 16; Length 139;
Pred. No. 8.7e-44;
5; Mismatches 9; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1; envelope protein E2; antibody; helper T-lymphocyte; IgG1; cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IgG1 antibody heavy chain variable region 15H4VH.
                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG67188 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                 82.4%; Scc.
83.7%; Pred
6; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-2000; 2000GB-0030102
18-DEC-2000; 2000GB-0030789
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                                                                                                                                                                                                                                                                                                                                                    Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-508540/54.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Sequence
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119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paraquat; antibody; light chain; herbicide; resistant; crop plant; weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I; free radical; lipid peroxidation; electron transport; photosystem II; vacuole; cell surface; cytotoxic; sensitive.
                                                                                                                                                                                                                                                                                        1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIY-WDDDK
                                                                                                                                                                                                                                                                                                               1 QVQLKESGPGILQPSQTFNQTCSFSGFSLSTSGMGVSWIRQPSGKGLDWLAHIYPWDDDK
                                                                                                                                                                                                                                                                                                                                                                    60 RYNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTV
                                                                                                                                                                                                                                                        Gaps
raising, in an infected individual, an antibody able to bind to the hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting HCV strain. The different groups of peptides are administered sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-lymphocytes which are cross-reactive to the HVR1 region of the infecting HCV. The vaccines are useful for preventing and treating chronic HCV infections. ABG67186-ABG67189 represent variable regions of human IgG1 antibody heavy chain.
                                                                                                                                                                                                                                                        4,
                                                                                                                                                                                                             82.1%; Score 520; DB 23; Length 121;
85.2%; Pred. No. 1e-43;
iive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicide binding proteins and related polynucleotides
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Best Local Similarity
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lipid peroxidation or by blocking electron transport in photosystem II. The herbicide binding proteins advantageously sequester the herbicide, e.g. at the cell surface or in the vacuoles of a treated plant. Sequestration at the cell surface prevents the entry of the herbicide into the cells or that the herbicide cannot reach its intracellular target and exert any significant cytoxic effect. The herbicide binding protein inhibits the mobility of the herbicide from the application site to the whole plant preventing the herbicide reaching particularly sensitive organs. Additionally, tolerant plants can be produced against herbicides that have more than one target site.
      electrons from photosystem I thus generating free radicals which cause
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ö 15; Indels Query Match
Best Local Similarity 81.8%; Pred. No. 2.6e-43;
Matches 99; Conservative 7; Mismatches 15; 1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60

121 8 121

121 \$ 121

Search completed: January 14, 2004, 19:11:24 Job time : 40.1905 secs

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Sequence 121 AA;

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ig heavy chain precursor V region (IdBS.7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: Pr0174
R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A;Title: Specificity and variable region CDNA sequence of an isogeneic monoclonal antiinh. A;Reference number: Pr0174; MUID:91287738; PMID:1712074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: FT0174
A;Molecule type: mRNA
A;Residues: 1-143 < PBE>
A;Experimental source: strain BALB/c
C;Comment: 1855.7 is an antibody to anti-alpha (1-6) dextran.
C;Souperfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin immunoglobulin
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Best Local Similarity
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633
1 QVTLKESGPGILQPSQTLSL......SLTAYAMDYWGQGTSVTVSS 121
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          283308 segs, 96168682 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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S26465
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Maximum DB seq length: 2000000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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474.5
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                                               OM protein
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                                                                                                                                                Sequence:
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leavy	Ig heavy chain V-I	eavy	neavy chain	neavy chain	neavy	neavy	neavy chain	≥ C72.	neavy						
PH1023	GIHUDW	S55028	530534	531512	831690	A32456	S52446	157810	S26324	830752	831514	844114	S19668	S78051	331586
N	Н	N	N	~	7	7	~	~	7	N	7	~	7	N	N
109	119	140	130	155	130	139	141	117	111	149	128	129	127	135	139
58.6	58.6	58.6	58.5	58.5								57.0	56.9	56.9	56.8
371	371	371	370.5	370	369	368.5	368.5	368	366	363	362	360.5	360	360	359.5
0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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C;Accession: S:1740
R;Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.
Submitted to the EMBL Data Library, May 1990
A;Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificition A;Reference number: S:11740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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Ig heavy chain precursor V-D-J region - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                          A,Accession: S11740
A,Accession: S11740
A,Molecule type: mRNA
A,Residues: 1-122 < ENBA
A,Cross-references: EMBL:X53097; NID:g52368; FIDN:CAA37261.1; PID:g762983
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 122;
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7; Indels
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DB 2; Length 143; Score 543.5; DB 2 Pred. No. 2.3e-44; 85.9%;

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Cyaccession: 33133 medicates of 1, Zouali, M. Rychaeternes of the EMBL Data Library, December 1992
Appearation: Dominance of clonotypic patterns and variable gene usage of anti-DNA autocyactiption: Dominance of clonotypic patterns and variable gene usage of anti-DNA autocyactiption: Dominance of clonotypic patterns and variable gene usage of anti-DNA autocyaction: Data Library Apacession: 331513
A; Reference number: 831503
A; Residues: preliminary
A; Ross-references: EMBL: X69861; NID: g33084; FIDN: CAA49495.1; PID: g33085
A; Cross-references: EMBL: X69861; NID: g33084; FIDN: CAA49495.1; PID: g33085
C; Superfemily: immunoglobulin numoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology < IMM>
                                                                                                                                                                                  Igheavy chain V region - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 (C) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 (State: State: State:
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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A,Residues: 1-116 <CTA>
A,Residues: 1-116 <CTA>
A,CTOSS-Teferences: EMBL:X59198; NID:G52074; PIDN:CAA41908.1; PID:g1334038
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;11-95/Domain: immunoglobulin homology <IMM>
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TISKDTSRNQVFLKITSVDTADTATYYCARRAGGYGNYGWYFDVWGAGTTVTV 113
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A;Molecule type: mRNA
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Proteins 14, 499-508, 1992
A;Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
A;Reference number: A49442; MUID:93066166; PMID:1438187
       5
                                                                                                                                                                                                                                                                           80 YNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYYCARRE--RGYGNYLGPLDYWGQGT 137
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                                                                             QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
                                                                                                                                                   20 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGRGLEWLAHISWDDDNL 79
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                                                                                                                                                                                                                            YNPSLKSRLTISKDISSNQVFLKIISVDTRDIATYYCARRVSLTAYA-----MDYWGQGT
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>
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       7;
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A/Residues: 1-107 <STU>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-91/Domain: immunoglobulin homology <IMM>
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Pred. No. 1.5e-39;
4; Mismatches 8;
       Mismatches
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Best Local Similarity 84.1%;
Matches 95; Conservative
           Conservative
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Best Local Similarity
Matches 92; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <KAV>
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           108;
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           Matches
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; Score 460; DB 2; ; Pred. No. 1.5e-36; 10; Mismatches 21

72.78;

Query Match Best Local Similarity

Best Loca Matches

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Molecule type: mRNA;Residues: 1-121 <REI>

90; Conservative

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Ig heavy chain precursor V region (BFL23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B25913
S;Lavler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A;Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A;Reference number: A94148; MUID:87175692; PMID:3104915
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C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C.Accession: 86939; 872664
R.Khamlichi, A.A.; A.A. a.Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Blochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition A;Reference number: 869339; MUID:952262687; PMID:7744049
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                                                                                                                                                                                                                                                                                                                                                              A;Cross-raferences: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.8%; Score 448; DB 2; Length 10 Best Local Similarity 85.9%; Pred. No. 1.7e-35; Matches 85; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCAR
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; Pred. No. 9.8e-34;
17; Mismatches 19;
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submitted to the EMBL Data Library, September 1994
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A;Residues: 1-140,'C',142-374 <KH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.4%;
Matches 83; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S72664
A;Accession: S72664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 1-374 <KHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Lg heavy chain V region (31-9D) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Jate: L2-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C.Jacession: 809959
V.Tecession: 809959
V.T. J. Immunol. 20, 771-777, 1990
V.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
V.Reference number: 809955, MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F. rthritis Rheum. 35, 900-904, 1992
Filtle: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene Reference number: A49002; MUID:92352481; PMID:1322670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTLKESGHGVLQPSQTLSLTCSVSGFSLSAHNMGVGWIRRPSGKGLEWLANIWMNDDKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
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Date: 19-bec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
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Experimental source: EBV-transformed lymphoblastoid cell line SSH23
Note: sequence extracted from NOBI backbone (NCBIN:110261, NCBIP:110262)
Superfamily: immunoglobulin v region; mmunoglobulin homology
Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X51847; NID:g55247; PIDN:CAA36140.1; PID:g930215 C5. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterctetramer; immunoglobulin P:15-99/Domain: immunoglobulin homology < IMM>
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RESULT 11

18; DB 2;

Query Match 71.8%; Score 454.5; DB 2 Best Local Similarity 70.2%; Pred. No. 5.1e-36; Matches 87; Conservative 16; Mismatches 18

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TVSS 121 TVSS 124

118 121

RESULT

15-99/Domain: immunoglobulin homology <IMM>

Molecule type: mRNA Residues: 1-124 <STU>

Status: preliminary

Accession: A49002

121 S 121 S 121

121

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Ig heavy chain V region precursor (VII-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C;Accession: 81855
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; F. F. Firble: Physical map of the 3' region of the human immunoglobulin heavy chain locus: classical and positive regions of the human immunoglobulin heavy chain locus: classical and procession and 
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R;Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W. J. Immunol. 126, 1212-1216, 1981
A;Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X A;Reference number: A02092; MUID:81118242; PMID:6780622
A;Accession: A02092
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C;Date: 14-Nov-1983 #sequence_revision 22-Nov-1983 #text_change 02-Sep-1997
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C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <WAT>
F;30-118/Domain: immunoglobulin homology <IMM>
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A;Map position: 14q32.33-14q32.33
S;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin proglutamic acid
F;15-99/Domain: immunoglobulin homology <IMM:
F;15-99/Domain: immunoglobulin homology <IMM:
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARR 100
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64.3%; Score 407; DB 1;
Best Local Similarity 63.2%; Pred. No. 1.6e-31;
Matches 79; Conservative 17; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 410; DB 2;
; Pred. No. 7.7e-32;
14; Mismatches 11
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Best Local Similarity 75.0%;
Matches 75; Conservative 1
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A;Residues: 1-119 <SHI>
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roc. Natl. Acad. Sci. U.S.A. 87, 6146-6150; 1990
.jttle: Preferential utilization of conserved immunoglobulin heavy chain variable gene;
Reference number: A36005; MUID:90349571; PMID:2117273
                                                                                                                                                        C.Accession: A02089
R.Press, E.M.; Hogg, N.M.
Biochem. J. 117, 641-660, 1970
A;Title: The amino acid sequences of the Fd fragments of two human gammal heavy chains.
A;Reference number: A90250; MUID:70258837; PMID:5449120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 14q32.33-14q32.33
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid
F;15-96/Domain: immunoglobulin homology <IMM>
F;17/Modified site: pyrrolladone carboxylic acid (Gln) #status experimental
F;22-94/Disulfide bonds: #status experimental
F;62/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
Date: 21-Dec-1990 #sequence_revision 13-Sep-1991 #text_change 16-Dec-1998
                                                                                         Species: Homo Bapiens (man)
Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-120 <PRE>
C;Comment: This chain was isolated from an IgG1 myeloma protein.
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A;Map position: 14q32.33-14q32.33
C)Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                  heavy chain V-II region (Cor) - human (tentative sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:128528; OMIM:147070
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Best Local Similarity 66.9
Matches 81, Conservative
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Molecule type: mRNA
Residues: 1-121 <SCH>
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61 YNPSLKSRLTISKDISSNOVFLKITSVDTRDTATYYCAR----RVSLTAYAMDYWGQGTS 116
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Ig heavy chain precursor V-II region (Cess) - human C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: A02090
R.Takahashi, N.; Noma, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 81, 5194-5198, 1984
A.Title: Rearranged immunoglobulin heavy chain variable region (V-H) pseudogene that del A.Reference number: A02090; MUID:84298107; PMID:6089186

A;Molecule type: mRNA A;Residues: 1-147 <TAK> A;Note: the sequence was determined from the differentiated gene A;Note: the authors translated the codon GGG for residue 16 as Trp, TGG for residue 142 as Ser, and CAG for residue 147 as Ser C;Genetics:

Gene: GDB:IGHV@

A)Cross-references: GDB:128528; OMIM:147070
A)Cross-references: GDB:128528; OMIM:147070
A)Chross-references: 163-3-14q32.33-14q32.33
A)Introns: 15/3
C)Cyperfamily: immunoglobulin V region; immunoglobulin homology
C)Seywords: heterotetramer; immunoglobulin
F):1-19/Domain: signal sequence #status predicted <SIG>
F):20-118/Region: V segment
F):20-118/Region: V segment
F):119-132/Region: D segment
F):119-132/Region: D segment

1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60 Gaps 7; Query Match 63.6%; Score 402.5; DB 1; Length 147; Best Local Similarity 62.3%; Pred. No. 5e-31; Matches 76; Conservative 16; Mismatches 23; Indels 7. ò

61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCA-----RRVSLTAYAMDYWGQ 113

20 QVNLRESGPALVKATHTLTLTCTFSGLSVNTRGMSVSWIRQPPGKALEWLARIDWDDDKY 79

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80 YGTSLETRLTISKDISKNQVVLKVINMDPADTATYYCARMQVIMVREVMITSNAFDIWGQ 139

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Search completed: January 14, 2004, 19:13:47 Job time: 17.2381 secs

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PIR; A02089; GHHUCO.

PIR; A02089; GHHUCO.

PIR; A02089; GHHUCO.

PIR; A02089; GHHUCO.

RO; GO:0003823; Frantigen binding activity; NAS.

GO; GO:000585; P:immune response; NAS.

RO; GO:0006955; P:immune response; NAS.

RICEPPO: IPR003100; Ig_MHC.

RICEPPO: IPR003306; Ig_MHC.

RICEPPO: IPR003306; Ig_MHC.

RICEPPO: IPR003596; Ig_W.

PEROSITE: PSS0835; IG_LIKE; I.

RWART; SMO046; Igy I.

PROSITE: PSS0835; IG_LIKE; I.

RWART; SMO0466; Igy I.

PROSITE: PSS0835; IG_LIKE; I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2004 (Human)
18-SEP-2004 (Human)
19-SEP-2004 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chains.";
Biochem. J. 117:641-660(1970).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                             P80419
P0110809
P011809
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13226 MW; 158A8B29AE7EEB98 CRC64;
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                                                                                             HV3V HUMAN
HV2O MOUSE
HV3N HUMAN
HV39 MOUSE
                                                                                                                                                                                                                                                                                        HV23 MOUSE
HV25 MOUSE
HV3S HUMAN
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MEDLINE=70258837; PubMed=5449120;
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P0172 P01825 P01871 P01771 P01771 P01771 P018532 P018522 P01852 P01852 P01852 P01852 P01852 P01852 P018
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P01770
P01807
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV43 MOUSE
HV2C HUMAN
HV2A HUMAN
HV46 MOUSE
HV44 MOUSE
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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633
1 QVTLKESGPGILQPS
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Match Length DB
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Perfect score:
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NON TER
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular basis for the temperature-dependent insolubility of cryoglobulins. X. The amino acid sequence of the heavy chain variable region of MCE.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                         21-JUL_1986 (Rel. 01, Created)
15-JUL_1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-II region MCE.
19 heavy chain V-II region CE.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81118242; PubMed=6780622;
Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 126:1212-1216(1981).
-!- MISCELLANBOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM CRYOIMMUNOGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02092; MHHUMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.3%; Score 407; DB 1; Length 125; Best Local Similarity 63.2%; Pred. No. 5e-35; Matches 79; Conservative 17; Mismatches 25; Indels
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PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13783 MW; 7A1ADF4C40F47BB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-August chain V-II region SESS precursor.
Homo sapiens (Human)
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                                                                                    STANDARD;
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125 AA;
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P04438;
                                                                                 HV2D HUMAN
P01817;
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HV2H_HUMAN
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61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCA-----RRVSLTAYAMDYWGQ 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QVNLRESGPALVKATHTLTLTCTFSGLSVNTRGMSVSWIRQPPGKALBWLARIDMDDDKY
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Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
"Subgroups of amino acid sequences in the variable regions of
immunoglobulin heavy chains"; Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
SEQUENCE FROM N.A.
MEDLINE=84298107; PubMed=6089186;
Takahashi N., Noma T., Honjo T.;
Takahashi N., Noma U., Honjo T.;
"Rearranged immunoglobulin heavy chain variable region (VH)
pseudogene that deletes the second complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V-II REGION SESS.
V SEGMENT.
D SEGMENT.
J SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 63.6%; Score 402.5; DB 1; Length Local Similarity 62.3%; Pred. No. 1.8e-34; es 76; Conservative 16; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;
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                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
PIR; A02090; G2HUCS.
HSSP; P01825; 7FAB.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005576; P:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-V.
Pfam; PF00047; Ig, 1.
PROSTIF; SMO0406; IGV.
Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
115-BEP-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
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P01818;
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Gaps

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CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE SERROW OF A PATTERNY WITH HYPERGAMMAGLOBULINEMIA.

CC -1- SIRRIUM OF A PATTERNY WITH HYPERGAMMAGLOBULINEMIA.

DR AND SPINE, A02091; GHUDW.

DR ASSP. POL798; LOKELTOON OF A CONTRACT OF A CONTRACT
                                                                                                                                                                                                                                                                                          61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAY-----AMDYWGQ 113
                                                                                                                                                                                                                                                                                                                           78 YNSTLKSRLITIKDNSKSQVFLKAMSLQTDDTARYYCA-SVSIYYYGRSDKYFTLDYWGQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 DKRYNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYÇARRVSLTAYAMDYWGQGTSV 117
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                                                                                                                                                                 1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                      20 QVQLKESGPGLVAPSQSLSITCTVSGFSL--TGYGVNWVRQPPGKGLEWLGTIWGNGSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
15-SPR-2003 (Rel. 01, Last sequence update)
15-SPR-2003 (Rel. 42, Last annotation update)
1g heavy chain V-II region DAW.
If heavy chain (Winan).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                    60.7%; Score 384; DB 1; Length 144; 60.9%; Pred. No. 1.4e-32; ive 17; Mismatches 23; Indels
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PYRROLIDONE CARBOXYLIC ACID.
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MEDLINE=70258837; PubMed=5449120;
                                    Query Match
Best Local Similarity 60.9%
Matches 78; Conservative
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Best Local Similarity
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P01816;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 RYNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSPSLKSRLTVTRDTSKNQVVLTMTNMDPVDTATYYCVHRHPRT-LAFDVMGQGTKVAV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAH-IYWDDDK 59
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MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980):
                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANBOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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                                                                                                                                                                                                                                                                                                                    Query Match 62.4%; Score 395; DB 1; Length 12
Best Local Similarity 61.5%; Pred. No. 8.3e-34;
Matches 75; Conservative 20; Mismatches 25; Indels
                                                                                                                                                             IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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121 AA; 13483 MW; 88A5082C273753B4 CRC64;
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                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region MOPC 141 precursor.
Mus musculus (Mouse).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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HSSP, P010825; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR03306; Ig MHC.
InterPro; IPR0356; Ig_V.
Pfam; PF00047; ig; 1.
InterPro; IPR003596; Ig_v.
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P01822;
21-JUL-1986 (Rel. 01, Created)
01-JUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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126 AA; 14276 MW; A85COBEODABC296F CRC64;
                                                                                                                            21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
119 heavy chain V-11 region OU.
Homo sapiens (Human).
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                                                                                  PRT;
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MEDLINE=89238351; PubMed=2497341;
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                                                                               STANDARD;
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121 TVTVSS 126
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Best Local Similarity
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                                                                            HV2A_HUMAN
P01814;
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                          RESULT 7
HV2A_HUMAN
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                                                                                                                                                                                                                                                                          SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                        ¥
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MEDLINE=74170779; PubMed=4524622;
Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
"Amino-acid sequence of the variable region of the heavy (alpha)
chain of a mouse myeloma protein with anti-hapten activity.";
Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
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MEDLINE=77244979; PubMed=268248;
MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANGOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
Rinfret A., Horne C., Dorrington K.J., Klein M.; "Cloning, sequencing and expression of the rearranged MOPC 315 gene segment."; A. M. 1. Immunol. 26:431-434 (1989).
                                                                                       [2]
SEQUENCE OF 1-31.
MEDLINE=78094475;
Jilka R.L., Pestka S.;
Jilka R.L., Pestka S.;
"Amino acid sequence of the precursor region of MOPC-315 mouse
"Amino acid sequence of the 74:5692-5696(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION MOPC 315.
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COMPLEMENTARITY-DETERMINING-3.
FRANKBOOKR-4.
BY SIMILARITY.
G -> GG (IN REF. 1; CAA30727).
G -> H (IN REF. 2).
GY -> YG (IN REF. 4).
N -> D (IN REF. 4).
MISSING (IN REF. 4).
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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Interpro; IPPR003106; Ig_MHC.
Interpro; IPPR003506; Ig_v.
Pfam; PP00047; ig; 1.
SWART; SW00406; iGv; 1.
PR0SITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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123
137
137 AA;
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Best Local Similarity
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; Pred. No. 9.2e-26;
18; Mismatches 39
                                                                                                                                                                                                                                                             21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
11g heavy chain V-II region WAH.
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01-FEB-1991 (Rel. 17, Last seq
15-SEP-2003 (Rel. 42, Last ann
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                                                                                                                                                                                                           STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                           HV2F HUMAN
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P20957;
         61
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                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLKESGPGLVAPSQSLSITCTVSGPSL--TGYGVNWVRQPPGKGLEWLGMIWGDGSTD 77
                                                                                       20 VQLQESGPGLVKPSQSLSLTCSVTGYSI - TSGYFWNWIRQFPGNKLEWLGFIKYDGSNGY
                                                                                                                                                                         62 NPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVSS
                                                        2 VTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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IG-LIKE.
   28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 327; DB 1;
64.3%; Pred. No. 7.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 01, Last sequence upda
(Rel. 42, Last annotation up
in V region PJ14 precursor.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00767; CAA24148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Conservative
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
>115
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15-SEP-2003 (Rel. 42,
Ig heavy chain V regi
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43CA; 24-JUL-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A02095; HVMS14.
1A7N; 29-APR-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1G7M; 17-JAN-01
PDB; 43C9; 24-JUL-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    HV44 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                         RESULT 9
HV44_MOUSE
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61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAY-----AMDYWG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YNPSLRGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYDIGTGSDDGIDVWG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RLQLQESGPGLVKPSETLSLTCIVSGGPIRRTGYYWGWIRQPPGKGLEWIGGVYYTGSIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVILKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Last Sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Alian V region XIG14 precursor (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                       MEDINE-82222235; PubMed-6806818; Tan L.-C., Putnam F.W.; Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.; "Complete amino acid sequence of the delta heavy chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
8
                                                                                                                                                                                                                                                   immunoglobulin D.";
Proc. Natl. Acad. Sci. U.S.A. 79;2850-2854(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AA; 14117 MW; DSD53D47ABE51319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PRIS, A02099; DZHVWA.
HSSP, POLBS5; FRWA.
GlycoSuiteDB; PO1824; -- GlycoSuiteDB; Po1825; P:immune response; NAS.
InterPro; IPR003105; Ig-like.
InterPro; IPR003596; Ig-like.
InterPro; IPR003596; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus
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9 9

Matches

à g 1;

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20 VQLQESGPGLVKPSQSLSLTCSVTGYSI-TSGYYWNWIRQFPGNKLEWMGYISYDGSNNY 78
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Kudo A., Ishihara T., Nishimura Y., Watanabe T.;

Kudo A., Ishihara T., Nishimura Y., Watanabe T.;

Rudo A., Ishihara T., Nishimura Y., Watanabe T.;

Tepadt sequence in S. Ishihara T., Stanking region.";

Gene 33:181-189(1985).

BIR, AGOIGLI, GHAUHA.

RHSSP, PO1825; Frantigen binding activity; NAS.

GO; GO:0003825; Frantigen binding activity; NAS.

RO; GO:0003825; Frantigen binding activity; NAS.

RO; GO:0003825; Frantigen binding activity; NAS.

RICETPO; IPR007110; 19-11.

RICETPO; IPR003596; Ig—V.

R PÉMN; PR00447; ig; 1.

R PROSITE; PS50835; IG—IKE; 1.

R RMART; SMO0406; IGV; 1.

R IMMUNOGIObulin V region; Signal.

T SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VILKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V-II region ARH-77 precursor.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 312.5; DB 1; Length 116; 60.2%; Pred. No. 2.4e-25; Live 18; Mismatches 20; Indels 1
                                                                                                                                                                                 IG HEAVY CHAIN V REGION M315.
PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 13095 MW; 4562E03E53DC9E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NPSLKNRISITRDISKNQFFLKLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 NPSLKSRLTISKDISSNOVFLKITSVDTRDTATYYCAR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update
                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-3.
BY SIMILARITY
                             Best Local Similarity 60.29
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the BNBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRYN 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                          MEDLINE=88176921; PubMed=2451244; Schwager J., Mikoryak C.A., Steiner L.A.; Schwager J., Mikoryak C.A., Steiner L.A.; Mikoryak G.A., Geduced "Amino acid sequence of heavy chain from Xenopus laevis 1gM deduced from cDNA sequence: implications for evolution of immunoglobulin domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.; "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response."; J. Exp. Med. 169:2007-2019(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION XIG14 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.8%; Score 315.5; DB 1; Length 52.1%; Pred. No. 1.4e-25; ive 20; Mismatches 34; Indels
                                                                                                                                                                                                                  domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15080 MW; EBC467105C00732E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA
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15-JUL-1999 (Rel. 38, Last annotation u
Ig heavy chain V region M315 precursor.
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; EF00047; ig; i. -3-...
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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InterPro; IRR07110; Ig-like.
InterPro; IRR03506; Ig_MHC.
InterPro; IRR03596; Ig_V.
FRam; PR00047; Ig' 1.
SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 52.1*
Matches 62, Conservative
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NCBI_TaxID=8355;
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IG HEAVY CHAIN V-II REGION ARH-77. V SEGMENT. D SEGMENT. J SEGMENT. BY SIMILARITY.
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                                                                                                    16228 MW; 8D7FD52BB218171F CRC64;
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Best Local Similarity 52.34
Matches 67; Conservative
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HSSP, P01825; 7FAB. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC.

DR REPRESENTED BY THE PROPERTY OF THE PROPERTY

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Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
"Amino acid sequence of the VH region of a human myeloma
immunoglobulin (IgG New).";
                                                                                                                                                             E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
11g heavy chain V-II region NEWM.
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Biochemistry 16:3412-3420(1977).
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126 AA;
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J. Mol. Biol. 141:369-391(1980).

C. - STRAILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02055; G1HUTA...

PIR; A02055; G1HUTA...

PIR; A02055; G1HUTA...

R PDB; 2FB4; 12-JUL-89.

R PDB; 2FB4; 12-JUL-89.

R QO; G0:0003823; F:antigen binding activity; NAS..

GO; G0:00059576; C:extracellular; NAS..

R InterPro; IPR0007110; Ig-like.

R InterPro; IPR003006; Ig-MrC..

R InterPro; IPR003006; Ig-MrC..

R InterPro; IPR003006; Ig-MrC..

R FROSITE; PSSC035; IG LIKE; I.

R SMART; SM00440; Ig; I.

R SMART; SM00440; Ig; I.

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                    21 QVQLQQWGAGLVKFSETLSLTCAVFGGSF--SGYYWSWIRQPPGRGLEWIGEINHSGSTN
                                                                   61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTA-----YAMDYWGQ
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MEDLINE=81289131; PubMed=6884994;
Schnidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
"Appe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81072295; PubMed=7441755; Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
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PRO GO: 0005576; C:extracellular; NAS.

GO: 00005576; C:extracellular; NAS.

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GO: 00005576; C:extracellular; NAS.

RO: 000005576; C:extracellular; NAS.

GO: 00005576; C:extracellular; NAS.

RO: 000005576; C:extracellular; NAS.

RO: 00000576; C:extracellular; NAS.

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BELLIKES 78066916, Pubmed=618887;
Saul F.A., Amzel L.M., Poljak R.J.;
"Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";
J. Boll. Chem. 253:585-597 (1978)
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                 11;
Query Match
48.4%; Score 306.5; DB 1; Length 126;
Best Local Similarity 50.4%; Pred. No. 1.1e-24;
Matches 65; Conservative 18; Mismatches 35; Indels 11;
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117 117
117 AA; 12790 MW; 2DA47B509562D237 CRC64;
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1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60 4; Gaps Query Match

48.2%; Score 305; DB 1; Length 117;
Best Local Similarity 49.6%; Préd. No. 1.4e-24;
Matches 60; Conservative 24; Mismatches 33; Indels

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Search completed: January 14, 2004, 19:11:51 Job time: 12 secs

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January 14, 2004, 18:55:07; Search time 36.6667 Seconds (without alignments) 851.574 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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61 YNPSLKSRLTISKDISSNOVFLKITSVDTRDIATYYCAR----RVSLTAYAMDYWGQGTS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QLQLQESGFQLVKSSETLSLTCTVSGGSISSSSYYMGWIRQPPGKGLEWIANTYYSGITY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLKESGPDLVAPSQSLSITCTVSGPALIS--YAISWVRQPPGKGLEWLGVIWTGGVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Momo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match

S8.5%; Score 370.5; DB 11; Length 482;
Best Local Similarity 61.2%; Pred. No. 3e-32;
Matches 74; Conservative 17; Mismatches 27; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 361.5; DB 4; Length 496; 59.2%; Pred. No. 3.1e-31; ive 17; Mismatches 29; Indels 5;
                                                                                          Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011181, AAH111811, -
InterPro; IPR00710; Ig-11ke.
InterPro; IPR00306; Ig-WC.
InterPro; IPR00306; Ig-W.
Pfam; PR00406; Ig-4.
SWART; SM00406; IG-4.
PROSITE; PS050835; IG-LIKE; 4.
PROSITE; PS050835; IG-LIKE; 4.
SROINGE 482 AA; 51865 MW; 312E01F9CIBC7F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
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Last annotation update)
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006, Ig_MHC.
InterPro; IPR003006, Ig_WHC.
InterPro; IPR003596, Ig_V.
Pfam; PF00047; ig; 4.
PROSITE; PS00359; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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Q96KX8;
01-DEC-2001 (TEMBLrel. 19,
01-DEC-2001 (TEMBLrel. 19,
01-MAR-2003 (TEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 59.2
hes 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                  SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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096KX8
0096KX8
0096KX
01-D)
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                                                                               61 YSPSLKSRLTITKDTSKNQVDLTMTFMDPMDTATYYCAHRKSGDGYYFDYWGQGTLVTVS 120
                                                  YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
     QITLKESGPTLVKPTQTLTLTCTFSGFSLTTSGMDVGWIRQPPGKALEWLALIYWDDDKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L., Bautsch W., Kola A., Klos A., Koehl J.;
"Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.",
J. Immunol. 160:2947-2958 (1998).
EMBL; AJ222550; CAA10890.1; -.
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLKESGPGLVAPSQSLSITCTVSGFPLTSH--GVSWVRQPPGKGLEWLGVIWGDGNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTA-YAMDYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 YHSALISKLSISKDNSKSQVFLKLNSLQTEDTATYYCARHYYKYANYAMDYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01DEC-2001 (TYEMBLrel. 19, Created)
01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
01-MAR-2003 (TYEMBLREL. 23, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 121
121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; I.
SMART; SM00406; IGV; I.
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Q99NG4;
01-JUN-2001 (TEMBLEEL: 17,
01-JUN-2001 (TEMBLEEL: 17,
01-MAR-2003 (TEMBLEEL: 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain Fv (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Plasmid pHEN1.
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Q91X92
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61 YNPSLKSRLTISKDISSNQVFLKITSVDIRDIATYYCARRV-SLTAYAMDYWGQGISVTV 119
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                                                                                                                                                                                                                                                                                                                            3 TLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRYN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Local Similarity 59.0%; Pred. No. 2.4e-30;
les 72; Conservative 16; Mismatches 31; Indels 3;
                                                                                                                                                                                                                                            56.2%; Score 356; DB 4; Length 97; 68.0%; Pred. No. 1.5e-31; ive 16; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; ARH11857.1; -.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-MHC.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_W.
PR08TT; SM0466; Igy; 1.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
11-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                           63 PSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCAR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TSLKSRLTISKDTSKSQVVLTMTNMDPMDTATYYCAR 97
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    EMBL; AF035802; AAB88534.1; -.
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                               Local Similarity
les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q96EY0
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Borretzen M., Natvig J.B., Thompson K.M.;

"Heterogenous RF structures between and within healthy individuals are not related to HLA DRB1*0401.";

Mol. Immunol. 0:0-0(1997).
                                                                                                                                                                                                                                                                        Homo gapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BEDLINES-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.0%; Score 361; DB 4; Length 119; 58.7%; Pred. No. 5.5e-32; trive 16; Mismatches 32; Indels
                                                                                                                                                                            119 119
119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Rheumatoid factor RF-ET13 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBL; AF035041; AAD56277.1; -.
HSSP; P01825; 7FAB.
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InterPro; IPR00306; Ig_MHC.
InterPro; IPR03506; Ig_V.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 71; Conserv
                                        VTVSS 143
117 VTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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01-MAY-2000
01-MAY-2000 (
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NON TER
SEQUENCE
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78 YNPSLKSRVTISVDTSKKQLGLKLSSVNAADTAVYYCARVITRASPGTDGRYGWDVWGQG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNPSLKSRLTISKDISSNQVFLKITSVDTRDIATYYCARRVSLTA-----YAMDYWGQG 114
                                                20 QVQLQQWGAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGBINHSGSTN 77
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukpetens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TAXID=9606;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-Lymph;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0029963; AAH02963.1; --
HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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Last annotation update)
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Interpro; IPR003006; Ig MHC.
Interpro; IPR003056; Ig_V.
Fam; PF00047; Ig. 5.
SMART; SM00406; IGV.
PROSTIE; PS0035; IG LIKE; 5.
PROSITE; PS00290; IG_WHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Ouer Jocal Similarity 55.30,
Best Local Similarity 55.30,
The Conservative Tip 
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                                                                                                                                                                                                                                                                                                                                                  TTVTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 TTVTVSS 144
                                                                                                                                                                                                                                                                                                      115 TSVTVSS 121
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Q9BU10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NPSLKORISITRDTSKNQFFLKLNSVTTEDTATYYCASR----GYSWFPNWGQGTLVTVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 VQLQESGPGLVKPSQSLSLTCSVTGYSI-TSGYYMNWIRQFPGNKLEMMGYINYDGSNNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VILKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-LYMPh;
SEQUENCE FROM N.A.
TISSUB-LYMPh;
Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; EC019235; AAH19235.1;
InterPro; IPR00710; Ig-like.
InterPro; IPR007106; Ig-MHC.
InterPro; IPR003596; Ig-V.
Ffam; PF00047; ig; 5.
SMART; SMO0406; IG-V.
PROSITE; PS00239; IG LIKE; 5.
PROSITE; PS00239; IG-MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.9%; Score 341; DB 4; Length 588; 55.9%; Pred. No. 6.9e-29; ive 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                      | Straubberg R.; | Strauberg R.; | Strauberged (19M-2001.1; - 18SP; | Pol810; 2FBJ. | 1.; | Straubperg. | Pol810; 2FBJ. | 1.; | Straubperg. | Pol810; 12-1ike. | InterPro; | IPR003006; | Ig_wHC. | InterPro; | IPR003006; | Ig_wHC. | InterPro; | IPR003006; | Ig_w. | SWART; | SM00406; | Ig_v. | SWART; | SM00406; | Ig_v. | SWART; | SM00406; | Ig_w. | PROSITE; | PS00835; | Ig_Like; 4. | PROSITE; | PS00209; | Ig_MC; 2. | PROSITE; | PS00209; | Ig_MC; 2
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QBWUX4,
QBWUX4,
QBWUX4,
QI-MAR-2002 (TIENBIRE1 20, Created)
O1-MAR-2003 (TIENBIRE1 23, Last sequence update)
O1-MAR-2003 (TIENBIRE1 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 588 AA, 64438 MM; FC60DBAD82B39FD7 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypotheital 52.0 kDa protein.
Mus musculus (Mouse).
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 71; Conserv
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q8WUX4

RESULT 9 Q8WUX4

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                                                                                                                                                                        PRELIMINARY;
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20 >150
150 150
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                          TSVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 YNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMDVWGQG 137
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                                                                                                                                                                                                                                                                                                                                                                                                 1 QVTLKESGPGILQPSQTLSLTCSPSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQQWGAGLLKPSETLSLTCGVYGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGSTN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLQQWGAGLIKPSETLSLTCGVXGGSF--SGYYWSWIRQPPGKGLEWIGEINHSGITN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; substituting the substituting of the substitution of the substituting of the substituting of the substituting substituting of the substituting of the substituting substitution substituting substitution substituting substituting substituting substituting substitution substituting substituting substituting substituting substitut
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55.9%; Pred. No. 1.5e-28;
iive 15; Mismatches 33; Indels
                                   Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AAH17356.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR003066; Ig-V.
InterPro; IPR003566; Ig-V.
Pfam; PR00407; ig; 5.
SMART; SM00406; IGV; I.
PROSITE; PS00359; IG LIKE; 5.
PROSITE; PS00290; IG-MHC; 3.
                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
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SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A. TISSUE=Muscle, and Lymph;
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Best Local Similarity
Matches 71; Conserv
SEQUENCE FROM N.A.
                      rissue=Lymph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS
                                                                                                                                                                               Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                         Sun C. H., Song C.-H., Lee C.-H., Lee S.-K.;
"Clonal proliferation of IgM secreting B cell in the synovium of Behcet's patient with arthritis.";
Submitted (OCT-1998) to the BMBL/GenBank/DDBJ databases.
BMBL; AF103795; AAC79084.1;
-INSEP; PO1825; FAA.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_W.
SMART; SM00406; IGy. 1.
SWART; SM00406; IGy. 1.
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VH4 HEAVY CHAIN VARIABLE REGION.
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
                                      150 AA
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Search completed: January 14, 2004, 19:13:12 Job time : 40.6667 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 DDKRYNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 DDDKRYNPSLKSRLTISKOTSSNQVFLKITSVDTRDTATYYCARRVSLT---AYA-MDYW 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLGRIYYRSKWY 60
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Jang Y.-J., Chung J., Park J.-Y.;
Jang Y.-J., Chung J., Park J.-Y.;
"Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX145445; AAN64329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR 2003 (TrEMBLrel. 23, Created)
U-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
Howe sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
foung D.C., \ensuremath{^{\prime}} . Whosin-reactive autoantibodies in rheumatic carditis and normal
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88.6%; Score 307.5; DB 4; Length 130;
Best Local Similarity 50.0%; Pred. No. 4.8e-26;
Matches 65; Conservative 20; Mismatches 36; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.4%; Score 331.5; DB 4; Length 122; Best Local Similarity 54.4%; Pred. No. 1e-28; Matches 68; Conservative 18; Mismatches 32; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AA; 13901 MW; 036131FC6EC1551E CRC64;
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122 AA; 13719 MW; 56CB0612586A6529 CRC64;
                                                                           llin. Immunol. Immunopathol. 87:184-192(1998).
BMBL; AF035039; AADS6275.1; -.
ISSP; P01825; 7FAB.
                                                                                                                                                                                                                                        Pfam; PF00047; 19; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q81ZD7
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Allowes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / WW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
US-09-764-304-2
US-08-290-592E-31
US-09-025-769B-33
US-09-025-769B-37
US-09-025-769B-61
PCT-US95-10033-27
PCT-US95-10033-27
US-09-205-231-59
US-09-205-231-61
US-09-205-231-61
US-08-253-501A-59
US-08-205-231-90
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US-08-205-231-90
US-08-205-231-90
US-08-535-501A-90
US-08-535-501A-90
US-08-535-501A-90
US-08-535-501A-90
US-08-535-501A-90
US-08-535-501A-91
US-08-535-501A-91
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
FILING DATE: 14-OCT-1993
FILING DATE: 14-OCT-1993
FILING DATE: 14-OCT-1993
PRIOR APPLICATION NUMBER: US 08/136783
FILING DATE: 07-SEP-1994
ATORNEY/AGENT INFORMATION:
NAME: SULTON, USEFFER-1994
ATORNEY/AGENT UNMBER: 94,028
REFERENCE/DOCKET NUMBER: 950186-3
TELECOMMUNICATION INFORMATION:
TELEPANE: (215) 270-5024
TELEPANE: (215) 270-5029
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 140 amino acids TYPE: amino acid TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-08-483-636-4
 470.5
467.5
459.5
454
    January 14, 2004, 19:10:12; Search time 15.1905 Seconds (without alignments) 337.028 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 QVTLKESGPGILQPSQTLSL.....SLTAYAMDYWGQGTSVTVSS 121
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-483-632-4

US-08-483-632-10

US-08-435-632-10

US-08-197-834-7

US-08-256-643-14

PCT-US-96-201A-29

US-08-553-501A-29

US-09-205-231-88

US-09-205-231-88

US-09-205-231-88

US-08-253-501A-29

US-08-436-463-17

US-08-436-463-17

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US-08-483-636-64

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                                                                                                                                                                                                                           328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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Match Length
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80 YNPSLKSRLTISKDTSSNQVFLKITSVDTADTATYYCARRETVFYWYRDVWGAGTTVTVS 139
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                                                                 1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                       20 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II4 Antibodies Useful in TITLE OF INVENTION: Treatment of II4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 569; DB 2; Length 141
Pred. No. 5.9e-50;
4; Mismatches 8; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property P.O. Box 1539 / UW2220 CITY: King of Prussia
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US/94/10308
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FILING APPLICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/11/366

FILING DATE: 07-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/136783

FILING DATE: 14-0c7-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 07-SEP-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTEXT: USA
ZIP: 19406-0839
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.1%;
Matches 109; Conservative
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amino acid
Matches 109; Conservative
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                                                                                                                                                                                                                                                      79
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                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence ", 58904
| Patent No. 5928904
| GENERAL INFORMATION: APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S. APPLICANT: Gross, Mitchell S. APPLICANT: Gross, Mitchell S. APPLICANT: Sylvester, Daniel R. I. APPLICANT: Sylvester, Daniel R. I. APPLICANT: Sylvester, 75
| TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF ENGURNES: 75
| CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
| CITY: King of Prussia STREET: P.A. GOUNTE: PA. COUNTE: PA. COU
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                                                          Score 569; DB 2; Length 140;
Pred. No. 5.8e-50;
4; Mismatches 8; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING YSYERM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-52P-193
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9CT/US/94/10308
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, JOHNIER: 950186-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.9%;
90.1%;
                                                             89.9%;
90.1%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 amino acids
amino acid
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                                                      Query Match
Best Local Similarity
Matches 109; Conserv
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Best Local Similarity
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TELEFAX: (
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US-08-483-636-4
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81 YNPSLKSRLTISKDTSSNQVFLKITSVDTADTATYYCARRETVFYWYFDVWGAGTTVTVS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SHIMAMURA, HARUMI
APPLICANT: HAMUNO:
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESSE: 9-C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: UP 028173/1993
FILING DATE:
INTERE.1993
ATTORNEY/AGRYT INFORMATION:
NAME: Oblon, No. 5639455man F.
REGISTRATION NUMBER: 10-661-0
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6e-49;
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Pred. No. 1.6
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US-08-436-463-14
; Sequence 14, Application US/08436463
                                                                                                                                                                                                                                        Sequence 7, Application US/08197834
Patent No. 5639455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERS: 24885 OPAT UR SEQUENCE CHARACTERISTICS: LENGTH: 246 ami-
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Best Local Similarity 89.6%;
Matches 112; Conservative
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MOLECULE TYPE: protein
US-08-197-834-7
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                                                     61 YNPSLKSRLTISKDISSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
                                                                                                  81 YNPSLKSRLTISKDISSNQVFLKITSVDTADTATYYCARRETVFYWYFDVWGAGTTVTVS 140
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21 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 80
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Pred. No. 5.9e-50;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08483632
Patent No. 5298904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniell R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDNIKA: 0.026

ZIP: 19406-0939

COMPUTER READABLE FORM: MEDIUM TYPE: RIOPPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTAME: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTAME: BATCHION DATA: APPLICATION NUMBER: US/08/483,632

FLING DATE: PETCHION DATA: APPLICATION NUMBER: US 08/117366

FLING DATE: 0.7-SEP-1993

PRIOR APPLICATION NUMBER: US 08/136783

FILING DATE: 14-0CT-1993

PRIOR APPLICATION NUMBER: PCT/US/94/10308

FILING DATE: 14-0CT-1993

PRIOR APPLICATION NUMBER: PS0186-3

FILING DATE: 0.7-SEP-1994

ATTORNEY/AGENT INFORMATION: NUMBER: 34,028

REFERENCE/DOCKET NUMBER: 35,028

TELESPAX: (215) 270-509

INPORMATION FOR SEQ ID NO: 10: SEGURENCE CHRAACTERISTICS: IDNOTATION OCIDES

INPORMATION FOR SEQ ID NO: 10: SEGURENCE CHRAACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property Treats: P.O. Box 1539 / UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.1%;
Matches 109; Conservative
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US-08-483-632-10
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STATE: P
COUNTRY:
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US-08-483-632-10
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APPLICANT: MAEDA, Hiroaki
APPLICANT: NESHIXAM, KIYOLO
APPLICANT: TOKLYOSHI, KIYOLO
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
OWNER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.1%; Score 551.5; DB 1; Length 122; Best Local Similarity 91.4%; Pred. No. 2.8e-48; Matches 106; Conservative 2; Mismatches 7; Indels 1.
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,463 FILING DATE: 26-JUN-1995 CLASSIFICATION NUMBER: US/08/436,463 FILING DATE: 26-JUN-1995 ATTORNEY APPLICATION NUMBER: 19 341255/1992 ATTORNEY/AGENT INFORMATION: NAME: YUN, Allen C. REGISTRATION NUMBER: 37,971 REPRENCE/COCKET NUMBER: KIMACHI=1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFRAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9507372
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ALIBORY SEQUENCES:
IS CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2000 One Allantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                           SEE: BROWDY AND NEIMARK, P.L.L.C.
19419 Seventh Street, N.W., Suite 400
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                            STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-07372-10
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STATE: Ge
COUNTRY:
ZIP: 303(
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61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
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US-08-533-501A-88
US-08-533-501A-88
Sequence 08 Application US/08533501A
Fatent No. 5856135
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
APPLICANT: HIRATA, Yuichi
APPLICANT: HIRATA, Yuichi
APPLICANT: BATO, Koh
APPLICANT: HIRATA, Yuichi
APPLICANT: BATO, Koh
APPLICANT: HIRATA, Yuichi
APPLICANT: ABOURNCES: 91
CORRESPONDENCES: 91
CORRESPONDENCE ADDRESS: ADDRESSE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 20..139
OTHER INFORMATION: /note= "Gln at position 20 starts
OTHER INFORMATION: mature peptide."
                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.5%; Score 522.5; DB 5
Best Local Similarity 84.3%; Pred. No. 2.7e-45;
Matches 102; Conservative 3; Mismatches 15
                                                                                                                                                                                                                                                                                                                   CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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ZIP: 20007-5109
COMPUTER READABLE FORM:
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COMPUTER: II
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                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 8 121
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61 YNPSLKSRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAY--AMDYWGQGTSVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGMTVGWIRQPSGKGLEWLAHIWWNDDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
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Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Massyuki
APPLICANT: SATO, Koh
ITILE OF INVENTION: RESIMBED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTELLEUKIN-6
NUMBER OF SEQUENCES:
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PECEDS/MS-DOS
SOFTWARE: PECEDS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATA:
FILING DATA:
APPLICATION: 536
CLASSIPECATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5-129787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 521.5; DB 3
Pred. No. 2.8e-45;
6; Mismatches 9
                     FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ATTORNEY AGENT: INFORMATION:
NAME: WEGNER, HAROId C:
REGISTRATION NUMBER: 25,258
REDERENCE/DOCKET NUMBER: 33466/177/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K Street, N.W., Suite 500 STAY: Washington
US/08/553,501
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202, ...
TELEFAX: 904136
; INFORMATION FOR SEQ.
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
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US-09-205-231-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGMTVGWIRQPSGKGLEWLAHIWWNDDKY 60
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Sequence 88. Application US/09205231

SENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: TSUCHIYA, Walchi
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-0058/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 J
FILING DATE: US/09/205,231
FILING DATE: US/09/205,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
          SCHAMING STAIRS | CLUCK/MS-DOS | CORRENT APPLICATION DATA; | CLASSIFICATION DATA; | SPELICATION DATA; | APPLICATION NUMBER: WD PCT/JP94/00859 | PILING DATE; 30-MAY-1994 | PILING DATE; 30-MAY-1994 | PILING DATE; 31-MAY-1993 | APPLICATION NUMBER: WD S-129787 | PILING DATE; 31-MAY-1993 | APPLICATION NUMBER: DS-129787 | TELECOMMUNICATION NUMBER: DS-129787 | TELECOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 521.5; DB 2;
Pred. No. 2.8e-45;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 88: SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-553-501A-88
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80 YNPALKGRLTISKDTSNNQVFLKIASVVTADTATYYCAR----MEDYDEAMDYWGQGTSVT 136
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                                                                                                                                                                                                                                                                                                                                                                20 QVILKESGPGILQPSQTLSLTCSFSGFSLNTSGMTVGWIRQPSGKGLEWLAHIWWNDDKY 79
                                                                                                                                                                                                                                                                                                                         1 QVTLXESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDXR
                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 5824307
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN, CECCHI, STEWART
ADDRESSEE: OLSTEIN
                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                      Length 139;
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                    Query Match 82.4%; Score 521.5; DB 3; Best Local Similarity 83.7%; Pred. No. 3.4e-45; Matches 103; Conservative 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWAREN FAPLICATION DATA:
APPLICATION NUMBER: US/08/290,592E
FILING DATE: ANGUET 15, 1994
CLASSIFICATION OATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Ellice M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
(202) 672-5300
(202) 672-5399
                                                                                                       LENGTH: 139 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 120 AMINO ACIDS TYPE: AMINO ACID
                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-994-1744
                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 139 amino aci
                                                                                                                                                              MOLECULE TYPE: protein US-09-205-231-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: PROTEIN US-08-290-592E-32
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 VSS 121
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    TELEPHONE:
                       TELEFAX:
TELEX: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YNPSLKSRLTISKDISSNQVFLKITSVDIRDIATYYCARRVSLTAY--AMDYWGQGTSVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 YNPALKGRLTISKDTSNNQVFLKIASVVTADTATYYCAR---MEDYDEAMDYWGQGTSVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVTLKESGPGILQPSQTLSLTCSFSGFSLNTSGMTVGWIRQPSGKGLEWLAHIWNDDKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                DB 2; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEB: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     ,4e-45;
                                                                                                                                                                                                                                                                                                                                             Score 521.5;
Pred. No. 3.4e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 5-129787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEGNER, Harold C.
REGISTRATION UNBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
TELECOMMUNICATION INFORMATION:
                                                                53466/177/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUKESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09205231
Patent No. 6121423
                NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 53466
TELECOMMINICATION INFORMATION:
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 : 139 amino acids
amino acid
                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 VŠŠ 139
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APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FELINE FRAGMENT CODING FOR SAID ANTIBODY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PGILOPSQTLSLTCSFSGFSLSTSGMG-SWIROPSGKGLEWLAHIYWDDDKRYNPSLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 PGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKRYNPSLKSR
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(7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 504; DB 1; Length 108; 90.8%; Pred. No. 1.4e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 LTISKDTSSNQVFLKITSVDTRDTATYYCARRV-SLTAYAMDYWGQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  Sequence 17, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08483636 Patent No. 5914110 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REPERENCE POCKET NUMBER: KI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Holmes, Stephen D. APPLICANT: Gross, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.89
Matches 99, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                              140 TVSA 143
                                  118 TVSS 121
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COUNTRY: US
ZIP: 20004
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                                                                                                                                                                          61 YNPSLKSRLTISKDISSNQVFLKIISVDIRDIATYYCARRVSLIAYAMDYWGQGISVTVS 120
                                                                                                                                                                                                            61 YNPSLKSRLTISKDISSNQVFLKIIGVDTADTATYYCARSM-ITNWYFDVWGAGTTVTVS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 YNPALKSRLTISKDTSSSQVFLKIASVDTADTATYFCVRSQIYFDYDGAWFPFWGQGTLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08436463
Patent No. 5760185
GENERAL INFORMATION:
APPLICANT: AFINACH:
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-FLINE HERPES VIRUS-1 RECOMBINANT
TITLE OF INVENTION: ANTI-FLINE HERPES VIRUS-1 RECOMBINANT
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street, N.W., Suite 400
                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVILKESGPGILQPSQILSLICSFSGFSLSISGMGAGWIRQPSGKGLEWLAHIWWDDVKR 79
                                                                         1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                        1 QVELQESGPGILQPSQTLSLTCSFSGFSLSTSGMSVGWIRQPSGEGLEWLADIWWDDXXD
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 143;
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     81.8%; Pred. No. 9.1e-44;
Live 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-UUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J7,971
REGISTRATION NUMBER: 37,971
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 1.4e-43;
6; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 143 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.8'
Matches 99, Conservative
Best Local Similarity 81.8 Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                      121 $ 121
                                                                                                                                                                                                                                                                                                                        120 $ 120
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APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant II4 Antibodies Useful in TITLE OF INVENTION: Recombinant II4 Mediated Disorders
NUMBERS OF SEGURES ADDRESS:
ADDRESSEE: SMITCHAILE DEFORERY
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1559 / WW2220
CITY: King of Prussia
COUNTRY: BAC OF PRUSSIA
COUNTRY: BAC OF PRUSSIA
COUNTRY: BAC OF PRUSSIA
CONFUTER: PA COUNTRY: BAC COUNTRY:
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Search completed: January 14, 2004, 19:14:23 Job time : 16:1905 secs

Sequence 2, Appliance 208, Appliance 208, Appliance 208, Appliance 218, Appliance 218, Appliance 24, Appliance 210, Appliance 210, Appliance 210, Appliance 241, Appliance 242, Appliance 244, Appliance 244, Appliance 246, Appliance 246, Appliance 246, Appliance 246, Appliance 246, Appliance 248, Appliance 27, Ap

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Sequence 7, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 4, Appli
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
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633
1 QVTLKESGPGILQPSQTLSL.....SLTAYAMDYWGQGTSVTVSS 121
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/IS06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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score greater than or equal to the score of the result bein
and is derived by analysis of the total score distribution.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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0 US-09-879-461-4

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1 US-09-995-529-12

2 US-110-010-942B-16

2 US-110-323-903-3

0 US-09-158-120A-32

0 US-09-158-120A-32

0 US-09-105-120A-32

0 US-09-105-13-4

1 US-10-011-931-3

US-09-764-304-4

2 US-10-265-74-304-4

5 US-10-265-73-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SMithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
SWedeland Rd.
                                                                                            Length 140;
                                                                                                                                                                                                                                                                                                                                                          ZIP: 19406-2799

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatchtIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FLICATION NUMBER: US/09/879,461
FLIANG DATE: 12-Jun-2001
CLASSIFICATION: <UNknown>
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89.9%; Score 569; DB 10;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 109; Conservative 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: «Unknown>
APPLICATION NUMBER: 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dification no. Care GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D. Gross, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09879461
Publication No. US20020193575A1
S-09-879-461-4
Sequence 4, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
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Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                   COUNTRY: USA

CONFUTER READABLE FORM:

MEDIUM TYPE: F10ppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHILD ROBER: US/09/879,461

FILICATION UNDERS: US/09/879,461

FILING DATE: 12-Jun-2001

CLASSIFICATION: <UNKNOWN>
                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220
Swedeland Rd.
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-995-529-12
Sequence 12, Application US/0995529
Sequence 12, Application US/0995529
Hublication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

89.9%; Score 569; DB 10;
Best Local Similarity 90.1%; Pred. No. 2.8e-48;
Matches 109; Conservative 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,929
FILING DATE: «Unchrown,
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1933
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acids
                                                                                 NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 8 121
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STATE: NI
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                          61 YNPSIKSRLTISKDTSSNQVFLKITSVDTADTATYYCARRANYGNPYYAMDYWGQGTSVT 120
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                                                                                                                                                                                                                                                     1 QVTLKETGPGILQPSQTLSLTGSFSGFSLSTSGMGVGWIRQPSGEGLEWLADIWWDDNKY 60
                                                                                                                                                                                                                         1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR 60
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                                                                                                                                                                                       Gaps
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                                                                                                                                          Score 555; DB 11; Length 123; Pred. No. 5.7e-47; 5; Mismatches 8; Indels
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Pred. No. 1.7e-46;
1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/10010942B
PUblication No. US20030165496A1
GENERAL INFORMATION:
APPLICANT: Baid, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Yedhock, Ted
APPLICANT: Yedhock, Ted
APPLICANT: Yedhock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA ANYLOID PEPTIDE
CURRENT APPLICATION NUMBER: US/10/010,942B
CURRENT FILING DATE: 2002-12-06
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SUFFRANCE SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10323903 Publication No. US20030228322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FISCHER, GERALD WALTER
                                                                                                                                          87.78;
87.88;
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87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.8<sup>†</sup>
Matches 108<sup>†</sup> Conservative
                                                                                                                                                             Best Local Similarity 87.8
Matches 108, Conservative
                                                     TYPE: PRT CRGANISM: Mus musculus US-09-995-529-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
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; LOCATION: (1)...(19)
US-10-010-942B-16
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                   SEQ ID NO 12
LENGTH: 123
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LENGTH: 142
                                                                                                                                          Query Match
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61 YNPSLKSRLTISKDISSNQVFLKITSVDTRDIATYYCARRVSLTAYAMD---YWGQGTSV 117
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Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against TITLE OF INVENTION: Respiratory Syncytical Virus NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & CASTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 525; DB 12;
Pred. No. 4.8e-44;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,120A
FILING DATE: September 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/613,372
FILING DATE: December 23,1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: P160
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SOFTWARE: MS Word 97
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 83.1%;
Matches 103; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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NEW JERSEY
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COUNTRY:
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                                          US-09-879-461-12
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US-10-011-931-3
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APPLICANT: ANDERSON, MAXMELL
APPLICANT: ANDERSON, SHERIE
APPLICANT: TEINH, IS TEINH
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APPLICANT: TEINH
APPLICANT: WINS, LETITA
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR PILING DATE: 1999-08-20
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                                                                                                                                                                                                                                                                                                                           2e-42;
                                                                                                                                                                                                                                                                                                  Query Match

80.0%; Score 506.5;

Best Local Similarity 81.8%; Pred. No. 3.2e

Matches 99; Conservative 7; Mismatches
                                                             469201-367
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Patent No. US20020068066A1
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
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SOFTWARE: PatentIn version 3.0
                                                                                                                 TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 120 AMINO ACIDS
TYPE: AMINO ACID
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Best Local Similarity 81.1:
Matches 99; Conservative
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MOLECULE TYPE: PROTEIN
US-09-158-120A-32
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; ORGANISM: Murine
US-09-881-823-8
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61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
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                                                                                                                                     APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant LL4 Antibodies Useful in
Treatment of LL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

COMPUTER: IN PC compatible

CORPUTER: IN CORPUTER: IN
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Best Local Similarity 76.9%; Pred. No. 1.1e-41;
Matches 93; Conservative 14; Mismatches 14; Indels
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-879-461-12
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Sequence 12, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/10011931; Publication No. US20030026806A1; GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 141 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: King of Prussia STAIE: PA
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SEQUENCE CHARACTERISTICS
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61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTA-YAMDYWGQGTSVTV 119
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                                                       1 QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDDDKR
                                                                                                  5 OVTLKESGPGILOPSOTLSLTCSFSGFSLSTYGMCVGWIROSSGKGLEWLANVWWSDAKY
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            Gaps
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US-10-166-626-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: MASEGRAM, MAMORU
APPLICANT: MYAJI, HIROMASA
APPLICANT: KUWANA, YOSHHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
            ;
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            20; Indels
          9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TURENT APPLICATION NUMBER: US/10/166,626
CURRENT APPLICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR PAPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-03-21
PRIOR PLING DATE: 1995-03-21
PRIOR PLING DATE: 1995-03-21
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1994-09-17
PRIOR APPLICATION NUMBER: US/07/947,674
PRIOR PLING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: US/07/947,674
PRIOR FILING DATE: 1991-09-18
PRIOR PLING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALCHIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10166626
Publication No. US20030166876A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.4%;
Matches 92; Conservative
          92; Conservative
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US-10-265-713-4
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                 APPLICANT: QIAN, ZUEMING
APPLICANT: QIAN, ZUEMING
APPLICANT: VEZINA, CHRIS
ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
TITLE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 60/244,118
PRIOR FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGGGTSVTVS 120
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APPLICANT: SHITARA, KENYA
APPLICANT: HANDAI, NOBON
APPLICANT: HANDAI, NOBON
APPLICANT: HANDAI, NOBON
APPLICANT: HANDAI, NOBON
APPLICANT: MIYALI, HIROMASA
APPLICANT: MIYALI, HIROMASA
APPLICANT: MIYALI, HIROMASA
APPLICANT: MIYALI, HIROMASA
APPLICANT: MUMANA, YORIHISA
TITLE OP INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERRACE: 249-101
CURRENT FILING DATE: 201-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-09-17
EARLIER FILING DATE: 1995-09-17
EARLIER FILING DATE: 1995-09-17
EARLIER FILING DATE: 1991-09-18
EARLIER FILING DATE: 1991-09-18
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es 13; Indels
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Pred. No. 1.1e-38;
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 499.5;
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Patent No. US20020026036A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Rat hybridoms
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 78
7 SOFTWARE: Patentin version 3.1
5 SEQ ID NO 3
1 LENGTH: 120
7 TYPE: PRT
0 ORGANISM: Wis musculus
US-10-011-931-3
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75.4%;
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Best Local Similarity 81.0%;
Matches 98; Conservative 5
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VARNUM, BRIAN C.
QIAN, ZUEMING
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SOFTWARE: Patentin Ver.
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LENGTH: 126
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61 YNPSLKSRLTISKDISSNQVFLKIISVDIRDIATYYCARRVSLIA-YAMDYWGQGISVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MANORU
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
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                                                                                                                                                                                                                                                                                             Length 141;
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                                                                                                                                                                                                                                                                                          DB 9;
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74.3%; Score 470.5; DB 5
Best Local Similarity 75.4%; Pred. No. 1.3e-38;
Matches 92; Conservative 9; Mismatches 20
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CURRENT PELICATION NUMBER: US/10/166,626
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR PLING DATE: 1996-03-10
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR PLING DATE: 1995-03-11
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1995-03-17
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1994-08-17
PRIOR PLING DATE: 1992-08-17
PRIOR PLING DATE: 1991-09-17
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Publication No. US20030166876A1
                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Rat hybridoma
US-09-764-304-2
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 141
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                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Matches 92; Conserv
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US-10-265-713-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHITAZA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MYAZI, HIROMASA
APPLICANT: KUWAXA, YOSHIHISA
IITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER PILING DATE: 1999-01-05
                                                                   APPLICANT: MIYAJI, HIROMSAA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REPERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 470.5; DB 15; Length 126;
Pred. No. 1.1e-38;
9; Mismatches 20; Indels 1;
                                                                                                                                                                                                   CURRENT RELIGION NUMBER: US/09/25,322
PRIOR APPLICATION NUMBER: US/09/25,322
PRIOR FILING DATE: 1999-01-05
PRIOR FILING DATE: 1995-03-1
PRIOR FILING DATE: 1995-03-1
PRIOR PRIOR PRIOR DATE: 1995-03-1
PRIOR PRIOR PRIOR DATE: 1995-03-1
PRIOR FILING DATE: 1995-03-1
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATCHIN VOWER: 2.0
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EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
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Patent No. US20020026036A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.41
Matches 92; Conservative
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Search completed: January 14, 2004, 19:25:04 Job time : 170:19 secs

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ω (σ, σ	80 6	877		E31225	E31225 Device for
o (σ, ο	88.	2		E30616	E30616 Antibody an
10	529	88.	NI		E30617	E30617 Antibody an
	50 6	87.8	ים	0	MUSL711GKV	M97875 Mouse hybra
	90.0	87.8	9	0	MUSL931GKV	M97879 Mouse hybri
	89	87.8	σ,	0	AF045518	AF045518 Mus muscu
	88	87.3	m		E07408	=
	88	87.3	m	Q	MMA005355	Mus mus
	88	87.3	ဖ	O	MUSL341GKV	onse
	86.	86.8	m		AR014069	Sequence
	86.	86.8	m	O	854207	S54207 V kappa 21=
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	86	86.7	Ŋ	0	MUSIGKABBC	M92401 Mouse Ig ka
	ω,	86.4	m	0	MUSIGLSB	M80406 Mouse Igh C
	ω .	86.4	m (0	542888	S428BB Ig V Kappa
	თ ∙	86.4	m 1		E02169	E02169 DNA encodin
	∞ .	86.4	m i	0	MMIGLC310	X65091 M.musculus
25	ω,	86.4	m	01	MMIGLC404	_
	∞ .	86.4	σ,	φ.	850265	٠.
	ω,	86.4	σ.	0	AF207705	AF207705 Mus muscu
	28	86.4	4 (N (AF402256	_
	•	85.9	ന	0	AY173024	
	83.	85.9	m	0	AF112403	
	83.	85.9	m	0	AF321952	Mus
	83.	85.9	m	0	MUSIGKAAW	louse
	83	82.0	σo 1		AR144017	Sequ
	81.	'n	m	10	MMU012372	Σ
	80.	'n.	9		MUSIGKAF	lus mu
	80.	85.1	0	v	I08223	ğ
	77.	4	S		MUSIGKABBH	onse
	27	ω.	3	10	MMVL1E10	louse mR
	27	83.6	IJ		MUSIGKABBD	onse
	75.	83.5	m		IGLC41	. muscu
	75	83.5	9	9	BD090559	Drug c
	S	83.5	9	ø	BD090668	Drug
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ALIGNMENTS

Antibody and nucleic acid encoding the same. B30643 B30643. B30643. B30643. B30643. B30643. B30643. B30643. B30643. B30643. B4066. B4066. B5066. B50

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A61P19/02, A61P29/00, A61P37/00, A61P37/06, A61P37/08, A61P43/00//
C12N15/09,
A61K37/02, C12N15/00
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Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I. Drug containing humanized anti-Fas antibody
Patent: JP 2001342148-A 2 11-DEC-2001;
                                                                                                                                                                               /gene="IgK"
(1.11). .363
/gene="IgK"
/gene="IgK"
feandard_name="L202; monoclonal antibody (CD4 antigen
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JP 2001342148-A/2
11-DEC-2001
28-MAR-2001 JP 2001093106
NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO
                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACATTGTGCTCACCAATTCTCCAGCTTCTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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ش
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                                                                                                                                     tissue_type="SP20-BALB/c fusion hybridoma"
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BD090542.
BD090542.1 GI:22636152
JP 2001342148-3/2
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                                                                                                                                                                                                                                                                                    82
                                                                            /sub_species="domesticus"
/db_xref="taxon:10090"
                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP 2001342148-A/2.
Mus musculus (house mouse)
Mus musculus
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96 c
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Best Local Similarity 94.6
Matches 315; Conservative
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AUTHORS
TITLE
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ORIGIN
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                                                                                                                    MITSUHARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08,
C12N15/00,
C12N15/00
Strandedness: Double;
Strandedness: Double;
Fopology: Linear;
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Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
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Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.

Lohman, K.L., Buck, D.W., Carrillo, M.A. and vennedy, R.C.

Lohman, K.L., diotope expression, and variable gene sequence unpublished (192)

Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.

Location/Qualifiers
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V-region; immunoglobulin light chain; immunoglobulin-kappa;
Processed gene.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                    /organism='Mus sp. (mouse)'. Location/Qualifiers
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Pred. No. 1.1e-88;
0; Mismatches 15
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
                     Mus sp. (mouse)
UP 1999332563-A/30
07-DEC-1999
26-MAY-1998 UP 1998163034
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PC A61P13/10 A61P13/
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C12P21/08//
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus.
1 (Dases 1 to 714)
Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ichikawa,K.,
Okuma,J., Otsuki,M., Shiraishi,A. and Yonehara,S.
Drug containing anti-Fas antibody
Patent: JP 200169393-A 2 20-JUN-2000;
SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIROKO YOSHIDA,
PI KIMIHISA ICHIKAWA,JUN OKUMA,MASAHIKO OTSUKI,AKIO SHIRAISHI,
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                                                                                                                                                                                                                                                                                                                                    Length 714;
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Pred. No. 1.2e-88;
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                                  /organism="Mus musculus"
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
a _184 c _173 g _157
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(61)..(714)
(1)..(60).
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            Location/Qualifiers
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Mus musculus (house mouse)
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JP 2000169393-A/2
20-JUN-2000
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Best Local Similarity 94.6%;
Matches 315; Conservative 0
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LOCUS
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2001342149-A 2 11-DEC-2001;
OS Mus musculus (mouse)
PD 11-DEC-2001;
PD 2001342149-A/2
PD 11-DEC-2001;
PD 11-DEC-2001
PF 28-MAR-2001 UP 2001093243
PI WATARU TAKHASHI,HIDEVUKI HARUYAWA,NOBUFUSA SERIZAWA PC A61P3/10, PC A61P1/10, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCTCCTGCAAGCCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAGAAACCAGGACACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAGAAACCAGGACAACCCAAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccrercaagaagaargcrecaaccrarracrercaacaaagraargaagarccrceg 360
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Takahashi, W., Haruyama, H. and Serizawa, N.
Drug containing humanized anti-Fas antibody
Patent: JP 2001342149-A 2 11-DEC-2001;
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ug containing humanized anti-Fas antibody
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Location/Qualifiers
(1) . (714)
L peptide (61) . (714)
G peptide (1) . (60)
Location/Qualifiers
1 . 714
/organism="Mus musculus"
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BD090651.
BD090651.1 GI:22636261

FP 2001342149-A/2.
Mus musculus (house mouse)
Musmusculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 293; DB 6;
Pred. No. 1.2e-88;
0; Mismatches 15
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/db_xref="taxon:10090"
_184 c 173 g 15
            Drug containing humanized
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Best Local Similarity 94.6%;
Matches 315; Conservative 0
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PAT 31-JAN-2002
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C12N15/09, AGIK38/00, AGIK39/00, AGIK39/395, AGIK39/395, AGIB37/00, PC
AG1P43/00,
PC C07K16/28, C12N1/21, C12N5/10, C12N15/02, C12P21/08/, (C12P21/08,
PC C12R1:91),
PC C12R1:91,
PC
                                                                                                                                                                                                                                                     61 GACATTGTGCTGACCCAATCTCCAGCTTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC 120
                                                                                                                                                                                                                                                                                                            61 ATCTCCTGCAAGGCCAGCCAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                          118 CAACAGAAACCAGGACAGCCAACCCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
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Takahashi, W., Haruyama, H. and Serizawa, N. Humanized anti-Fas antibody
Patent: JP 2000166573-A 2 20-JJN-2000;
                                                                                                                                                                                                 1 GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                          3; Gaps
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                                                                                     Length 714;
                                                                               Query Match

88.8%; Score 293; DB 6; Length 714
Best Local Similarity 94.6%; Pred. No. 1.2e-88;
Matches 315; Conservative 0; Mismatches 15; Indels
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/db_xref="taxon:10090"
_184 c 173 g
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JP 2000166573-A/2
20-JUN-2000
29-SEP-1999 JP 1999275440
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   173 9
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JP 2000166573-A/2.
      184 c
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sig_peptide
200 a
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BASE COUNT
ORIGIN
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TITLE
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SOURCE
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E43359
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C12N1/21,C12NS/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
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CIZNI5/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 714)
Scrizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Humanized anti-Fas antibody
Patent: JP 2000166574-A 2 20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGGATCCCAGCCAGGTTTAGTGGCAGTCTGGGACAGACTTCACCCTCAACATCCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
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                                                                                                                                                                                                                                                                                                                                                                                            61 GACATIGIGCIGACCCAATCICCAGCTICTTIGGCTGTGTCTCTAGGGCAGAGGCCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
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                                                                                                                                                                                                                   88.8%; Score 293; ______
94.6%; Pred. No. 1.2e-88;
tive 0; Mismatches 15; Indels 3; Gaps
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                           1. 714
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
a _184 c 173 g 157
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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JP 2000166574-A/2
20-JUN-2000
29-SEP-1999 JP 1999275441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F40813
Humanized anti-Fas antibody.
   Location/Qualifiers
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JP 2000166574-A/2.
Mus musculus (house mouse)
                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.6%
Matches 315; Conservative
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ORIGIN
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AUTHORS
TITLE
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E40813
   FEATURES
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linear PAT 18-JUN-2001
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C12N15/02,A61K39/395,A61K39/395,C07K16/28,C12N15/09,C12P21/08,
C12N15/00,
C12N15/00
Strandedness: Double;
                                                                                                                                                                                         199 GGGATCCCAGCCAGGTTAGTGGCAGTGGGGTCTGGGACAGACTTCACCCTCAACATCCAT 258
    19 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC 138
                                                                                                      178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTTCTGGGACAGACTTCACCTCAACATCCAT 237
                                                                                                                                                                                                                                                      238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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Mitanharu,O., Takayuki,K. and Ikuo,M.
Antibody and nucleic acid encoding the same
Patent: JP 1999332563-A 3 07-DEC-1999;
ASAHI CHEM IND CO LTD
                                                                         118 CAACAGAAACCAGGACAACCAAAACTCCTCAACTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                               259 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAGTGAGGATCCTCCG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.88.88; Score 293; DB 6; Length 92
Best Local Similarity 94.68; Pred. No. 1.2e-88;
Matches 315; Conservative 0; Mismatches 15; Indels
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Antibody and nucleic acid encoding the same.
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
/236 c 268 g 19
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JP 1999332563-A/3
07-DEC-1999
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TITLE
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                                                                                                                                                                                                       180
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Mitsuharu, O., Takayuki, K. and Ikuo, M.
Morice for separating CD4-positive cells and separation method Patent: JP 199932594-A 3 07-DEC-1999;
ASAHI CHEM IND CO LID
                                                                                                             61 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCACC 120
                                                                                                                                                         61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
                                                                                                                                                                                                                                                 118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                            181 CAACAGAAACCAGGCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 240
                                                                                                                                                                                                                                                                                                                                      178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
                                                                                                                                                                                                                                                                                                                                                                                241 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                            238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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                                                                    1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAAGGGCCACC
                                                                                                                                                                                      3; Gaps
                             3; Gaps
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PN JP 1993312544-A/3
PN JP 1993312544-A/3
PP 26-MAX-1998 JP 1998163023
PR MITSUHARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
PC C1201/04, CO7K16/28, CO7K16/46, C12M1/34, G01N33/53 CC
Strandedness: Double;
CC Topology: Linear;
FT Key Location/Qualifiers
FT Source (or 1.877)
FT FY (mouse)'.
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    94.6%; Pred. No. 1.2e-88;
ive 0; Mismatches 15; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:10095"
_219 c 255 g 18
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Matches 315; Conservative
Best Local Similarity 94.6
Matches 315; Conservative
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MUSL/11GKV 354 bp mRNA linear ROD 29-OCT-1994
Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial
                                                                                                                                                                                                                                                                               V-region; Unimizer, V-region; Immunoglobulin-Kappa; processed gene.

Mus musculus (house mouse)

Lokare, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.

Characteriation of murine monoclonal anti-CD4; epitope

recognition, idictope expression, and variable gene sequence
706 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAGTGAGGATGCTCCTCCG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATCTCCTGCAAGGCCAACCCAAAGTGTTGATTATGATGGTGATAGTTATATATG---TGGTAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CAACAGAAACCAGGCAGCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGGATCCCAGCCAGGTTTGGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="IgK"
/standard_name="L71; monoclonal antibody (CD4 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 289.8; DB 10; Length 354; 94.0%; Pred. No. 1.4e-87; 1ve 0; Mismatches 17; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="SP20-BALB/c fusion hybridoma"
                                                             298 ACGITCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
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/strain="BALB/c"
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CI2N15/02,A61K39/395,A61K39/395,CO7K16/28,C12N15/09,C12P21/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (20 925)
Mitsuharu, O., Takayuki, K. and Ikuo, M.
Antibody and mucleic acid encoding the same Parent: JP 1999332563-A 4 07-DEC-1999;
                                         238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
                                                                                                                         466 GACATTGTGCTGACCCAATCTCCAGCTTCTTGGCTGTGTCTCTAGGGCAGAGGGCCACC 525
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                   178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 237
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Antibody and nucleic acid encoding the same.
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/db_xref="taxon:10095"
236 c 268 g 19
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JP 1999332563-A/4
07-DEC-1999
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JP 1999332563-A/4.
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/mol_type="mRNA"
/strain="CSTBL6"
/db_xref="taxon:10090"
/chromosome="6"
/clone="SG6"
/cll_line="spleen cell hybridoma"
/1. .3391
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region, (IgK) mRNA, partial cds.
AF045518
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                                                                          Mus musculus (house mouse)
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                                     AF045518.1 GI:2906119
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/gene="1gK"
358. .>393
/gene="1gK"
a 100 c
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'gene="IgK"
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Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C. Characterization of mutine monoclonal anci-CD4; epitope recognition, idiotope expression, and variable gene sequence Unpublished (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGT---TGGTAC 117
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Mus musculus 5G6 monoclonal antibody kappa light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="IgK"
/standard name="L93; monoclonal antibody (CD4 antigen
specificity)"
97  89   83 t
                                                                                                                                                                                                                                                                                                                                                                   Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                            M97879.1 GI:198681
V-region; immunoglobulin light chain; immunoglobulin-kappa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="SP20-BALB/c fusion hybridoma"
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0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sub_species="domesticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                             processed gene.
Mus musculus (house mouse)
Mus musculus
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/strain="BALB/c"
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/tränslation="metotilimvillimvegstgdivltgspaslavslagratisck
asgsvdydgdsymnwyqokpqpppkiliyaasnlesgiparfsgsgsgtdftlnihpv
Eeedaatyycqqsnbdpwtfgggtklbik"
Sukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 393) (bases 1 to 393) (bases 1 to 393) (bases 1 to 394) (bases 1 to 304) (barielly Rarielly R.C., Farrelly T.P., Morikawa, A. and Stollar, B.D. Anti-DNA antibodies of normal mice immunized with poly(GC) are structurally similar to natural autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                   O'CONDOT, K.C., Fazrell, T.P., Morikawa, A. and Stollar, B.D.
Direct Submission
Submitted (02-FBE-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
Location/Qualifiers
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94.0%; Pred. No. 1.4e-87;
tive 0; Mismatches 17; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="monoclonal antibody kappa light chain"
protein_id="AAC04546.1"
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Monnet,C., Laune,D., Laroche-Traineau,J., Biard-Piechaczyk,M., Briant,L., Bes,C., Pugniere,M., Mani,J.C., Pau,B., Cerutti,M., Bevauchelle,G., Devaux,C., Granier,C. and Chardes,T. Synthetic peptides derived from the variable regions of an anti-CD4 monoclonal antibody bind to CD4 and inhibit HIV-1 promoter activation in virus-infected cells 91211214
                                                                                                                                                                     ROD 08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-APR-1998) Chardes T., Faculte de Pharmacie, CNRS UMR
9921, 15 Avenue Charles Flahault - Montpellier, 34060, FRANCE
Location/Qualifiers
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                    333 bp mRNA linear ROD Mus musculus immunoglobulin variable light chain region. AJ005355
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/note="anti-CD4"
                                                                                                                                                                                                                                     AZ005355.1 GI:3046765
immunoglobulin; light chain; variable region.
298 ACGITCGGIGCIGGACCAAGCIGGAGCIGAAA 330
                             301 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 333
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/cell_line="F142-63/ST40"
/cell_type="hybridoma"
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/mol_type="mRNA"
/strain="balb/c"
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Unpublished
3 (bases 1 to 333)
Chardes, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Mus sp.'
/clone='mu 5.5'
1. .333
/product='L chain variable region of mouse FT anti-HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                    E07408 333 bp RNA linear PAT 29-SEP-1997 CDNA encoding L chain variable region of mouse anti-HIV antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CAACAGAAACCAGGACAGCCAACCCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 180
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 333) Maeda. H., Kurumi, K., Eda, Y., Shiosaki, K., Nagatomi, K. and Tokiyoshi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1991 JP 1991359808
MAEDA HROAKI, KURUMI KARJUHKC, EDA YASUYUKI, SHIOSAKI
HI, PI NAGATONI KIYOSHI, TOKIYOSHI YUKIO
C12P21/08,A61K39/395,A61K39/395,C12N15/13,(C12P21/08, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          RECOMBINANT ANTI-HIV ANTIBODY AND ITS PREPARATION PATENT: JP 1994125783-A 4 10-MAY-1994; CHEMO SERO THERAPEUT RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
361 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393
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/organism="Mus sp."
/mol_type="genomic RNA"
/db_xref="taxon:10095"
a 83 c 86 g 76
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JP 1994125783-A/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            topology: Linear;
hypothetical: No;
                                                                                                                                                                                       E07408.1 GI:2175547
JP 1994125783-A/4.
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C12R1:91);
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a
                                                                                                                                                                  E07408
                                                                                                                                         DEFINITION
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                                                                      RESULT 14
E07408
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                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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        Qy
        238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCC 297

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        241 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCGTGG 300

        Qy
        298 ACGTTCGGTGCTGGAGCTGAAACTGAAA 330

        Db
        301 ACGTTCGGTGCACCAAGCTGGAATCAAA 333
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Search completed: January 14, 2004, 17:00:19 Job time : 1625.9 secs

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Murine Mab 187 lig
Murine Mab 187 lig
Mouse Mab 389 ligh
Light chain variab
Light chain coding
Antibody 4HS L cha
Murine derived DNA
Anti-Fas Mab HFE7A
                                                                                                                                                          January 14, 2004, 14:23:59 ; Search time 169.524 Seconds (without alignments) 5254.805 Million cell updates/sec
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/ SIDS1/gcgdata/gcneseq/geneseqn-emb1/NA1984.DAT:
/ SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:
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2: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT;*
3: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5105512
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2552756 segs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAL4861
AAQ83490
AAX85884
AAX79519
AAZ58690
AAZ58690
                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                               US-09-759-112A-22
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Maximum DB seq length: 200000000
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CDNA encoding mous Murine anti-Fas an Mouse humanised an Humanised anti-Fas Antibody 4H5 L Cha Antibody 4H5 L cha Murine derived DNA Murine derived DNA	in HIV antibo encoding mo an penton ba an penton ba encoding mo e fragment o i-CP4 antibo chi region	monocional an 1-Leu 3a light 1-SAF-1 monocil 1-Pas humanise encoding huma anised anti-Fa anised anti-Fa anised anti-Fa anised anti-Fa inc derived DN 1-Pas humanise	Anti-Fas numanised DNA encoding human DNA encoding human Humanised anti-Fas Humanised HFE7A de Humanised anti-Fas Humanised anti-Fas Humanised anti-Fas
04000000	2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	WW470048007	AA770078 AAA72125 AAA72125 AAA11615 AAA11615 AB145942 AB148685 AB148685
444444444	4 H H G G G H H H H H H H H H H H H H H	8129122222	222222222
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ALIGNMENTS

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New polynucleotide encoding a complementarity- or framework-determining
                                                                                                               Mouse, 1F7, antibody, immune modulator, anti-HIV antibody, CDR, complementarity determining region, framework-determining region, FR, heavy chain, light chain, HIV infection, gene, ss.
                                                                                         Murine Mab 1F7 light chain coding sequence.
                      AAL48660 standard; DNA; 330 BP
                                                                                                                                                                                                                                    11-JAN-2002; 2002WO-US00927.
                                                                                                                                                                                                                                                           11-JAN-2001; 2001US-0759112.
                                                                     11-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                 (IMMP-) IMMPHERON INC.
                                                                                                                                                                                                                                                                                                       Muller S, Kohler H;
                                                                                                                                                                                                                                                                                                                             WPI; 2002-590668/63.
                                                                                                                                                                                      WO200255668-A2.
                                                                                                                                                                                                              18-JUL-2002.
                                              AAL48660;
                                                                                                                                                                Mus sp.
RESULT 1
             AAL48660
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The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 light chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 Gridoaddaddaddrigcaaccrarracrercagcrrrgraardaggarccreccace 300
                                                                                                                                                                                                                                                                                New polynucleotide encoding a complementarity- or framework-determining region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGTGGTACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAAACCAGGACAGCCAACCTCCTCACCTATGCTGCATCCAATCTAGAATCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 330; DB 24;
100.0%; Pred. No. 2.1e-92;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 330 BP; 80 A; 87 C; 83 G; 80 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 23; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ83490 standard; cDNA; 396
                           11-JAN-2001; 2001US-0759112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 100.
330; Conservative
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/*tag=
                                                                               (IMMP-) IMMPHERON INC
                                                                                                                                                                                                                                                                                                                                                                  vaccines against HIV
                                                                                                                                                                                                WPI; 2002-590668/63.
                                                                                                                                         Kohler
                                                                                                                                                                                                                            P-PSDB; AA018536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
20-SEP-1995
                                                                                                                                      Muller S,
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                                                                                                                                                                              The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primat anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 light chain
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region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV
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Pred. No. 2.1e-92;
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/product= "1F7 light chain"
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/note= "no start or stop codon"
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                                                                                                                             Claim 10; Page 22-23; 27pp; English.
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Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction Immunoglobulin E-mediated allergic reaction, allergic rhinitis; conjunctivitis, atopic dermatitis; atopic asthma; anaphylattic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                               Light chain variable region cDNA of murine IL-4 antibody 3B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA molecules encoding recombinant antibodies useful treating IL4-mediated conditions
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P-PSDB; AAY23767.
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07-SEP-1994;
      13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. CDMA clones of the 3B9 light and heavy chains were cloned into pGEM7f+ and transformed into E. coli DH5.alpha. The clones were sequenced (AAQ83490-91), and used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%; Score 294.6; DB 16; Length 396; 94.9%; Pred. No. 2.2e-81; ive 0; Mismatches 14; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                            BEECHAM CORP.
BEECHAM PLC.
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93US-0136783.
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                                                                                                                                                                                     07-SEP-1994;
                                                                                                                                                                                                                               07-SEP-1993;
14-OCT-1993;
                                                                                                  WO9507301-A1
sig_peptide
                                        mat_peptide
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The present sequence encodes the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monotonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic resonunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. b BLISA of circulating endogenous IL-4 levels in humans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 396 BP; 99 A; 103 C; 103 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316; Conservative
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AAX85884 standard; cDNA; 396

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117
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                              GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                          241 egearcccaeccaegririaereecaerecercreecacaeacaecricaecercaacar
                                                                                        CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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 181 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides an antibody having affinity to CD4 antigen. Th anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the antibody 4H5 L chain fragment encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 6.6e-81,
0, Mismatches 15, Indels
                                                                                                                                                                                                                                                                                                                                                   Antibody 4H5 L chain fragment encoding nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 333 BP; 87 A; 86 C; 84 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                CD4 antigen; anti-human; antibody; 4H5; drug; ds
                                                                                                                                                   298 ACGITCGGIGCIGGACCAAGCIGGAGCIGAAA 330
                                                                                                                                                                              ACGTICGGIGGAGGCACCAAGCIGGAAAICAAA 393
                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                          AAZ58690 standard; cDNA to mRNA; 333
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al Similarity 94.6%;
315; Conservative
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Best Local S
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                                                                                                                                                                                                                                                     Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy; autolmmune disease; graft versus host disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes the light chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic astma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                           for murine 3B9 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 294.6; DB 20
94.9%; Pred. No. 2.2e-81;
live 0; Mismatches 14
                             298 ACGITCGGIGCTGGACCAAGCTGGAGCTGAAA 330
                                                          361 ACGITCGGTGGAGGCACCAGCTGGAAATCAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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93US-0117366.
93US-0136783.
94WO-US10308.
                                                                                                                                  standard; cDNA; 396
                                                                                                                                                                                                                           chain coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0483636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant IL4 antibodies
                                                                                                                                                                                              (first entry)
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Best Local Similarity 94.9
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-370482/31.
P-PSDB; AAY18120.
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07-SEP-1993;
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07-SEP-1994;
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301
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                                                                                                                                GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                             181 GGGATCCCAGCCAGCTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                                                                 CCTGTGGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTTGTAATGAGGATCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPETA, monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFETA; autoimmune disease; Hashimoto's disease; systemic lupue erythematosus; graft versus host disease; sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; attoriosclerosis; myocarditis; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy; ds.
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Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference Example 4; Page 188-189; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  298 ACGTTCGGTGCTGGACCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 333
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97JP-0082953.
97JP-0169088.
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(first entry)
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25-JUN-1997;
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15-MAR-1999
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118
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AAV1030
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                                                                    241 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAGTGAGGATCCTCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD4 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence encodes a murine derived protein fragment which is used to illustrate the method of the invention.
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Pred. No. 6.6e-81;
0; Mismatches 15; Indels 3
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                                                                                                                                                                                                        301 ACGTTCGGTGGAGCACCAAGCTGGAAATCAAA 333
                                                                                                                                                      298 ACGITCGGIGCIGGGACCAAGCIGGAGCIGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soka T, Morimoto I, Miyamura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine derived DNA fragment #6.
                                                                                                                                                                                                                                                                                                                                                                                           AAZ44232 standard; DNA; 333 BP
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(ASAH ) ASAHI MEDICAL CO LTD
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Best Local Similarity 94.6%;
Matches 315; Conservative
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98JP-0163023
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XX AAZ AAZ4
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This nucleotide sequence codes for the light chain (see AAW83042) of murine anti-human Fas monoclonal antibody HFE7A. The cDNA was contained from HFE7A secreting hybridoma cells (FERM BP-9818) by FATPCR (see AAV70127-28). The invention provides humanised versions of HFE7A (see AAW83031-37) which, like HFE7A, are capable of inducing apoptosis in abnormal cells. The humanised antibodies has in adminised antibodies are used to evaluate, in animal models, treatments of diseases that involve Pass/Pas lidgand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Habilmoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple solerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergias, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 293; DB 19; Length 714; Pred. No. 8.5e-81; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding mouse anti-Fas antibody HFE7A light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGITCGGIGCIGGACCAAGCIGGAGCIGAAA 330
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Matches 315; Conservative
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA.

Or a humanised version of HFETA containing identical CDRs interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, arcopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents cDNA encoding the light chain of the murine anti-human Fas monochonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
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                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CAACAGAAACCAGGACAGCCACCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas, antibody, murine, anti-inflammatory, anti-anemic, antidiabetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.8%; Score 293; DB 21; Length 714; 94.6%; Pred. No. 8.5e-81; ive 0; Mismatches 15; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine anti-Fas antibody HFE7A light chain cDNA
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                                                                                                                                                                                                                                                                                     Example 4; Page 69-70; 139pp; Japanese
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                                                         98JP-0276883
                   99JP-0278301
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Matches 315, Conservative
                                                                                                SANY ) SANKYO CO LTD
                                                                                                                                        WPI; 2000-485645/43.
                                                                                                                                                                                                                                                anti-Fas antibody
                                                                                                                                                            P-PSDB; AAB14748
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                   30-SEP-1999;
                                                         30-SEP-1998;
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Pas; perpropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFETA; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgan's syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                                                                                                                                                                                                      Tamaki I, Takahashi
                                                                                                                                                                                                                                                      Nakahara K,
                                                                                                                                                                               99EP-0307711.
                                                                                                                                                                                                   98JP-0276881
                                                                                                                                                                                                           98JP-0276882
                                                                                                                                                                                                                                                     Serizawa N, Haruyama H,
                                                                                                                                                                                                                                (SANY ) SANKYO CO LID.
                                                                                                                  Mus musculus
                                                                                                                                                                              29-SEP-1999;
                                                                                                                                                                                                   30-SEP-1998;
                                                                                                                                                                                                             30-SEP-1998;
                                                                                                                                     EP990663-A2
                                                                                                                                                          05-APR-2000
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New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively icells with abnormal Fas-Fas ligand systems 2000-258930/23. P-PSDB; AAW90898

Example reference 4; Page 102-103; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cells with an abnormal Fas/Fas apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, and transplant rejection. (1) selectively antibit apoptosis in normal cells will rejection. (1) selectively inhibit apoptosis in normal cells will rejection. (1) selectively inhibit disease models. (1) and transplant rejection. (1) selectively inhibit disease models. (1) and transplant rejection. (1) selectively inhibit disease models. (1) and transplant rejection. (1) selectively inhibit disease models. (1) act on the active site of Fas, i. e. they minic the native ligand, do not induce liver disease, and have reduced in the attive ligand, anti-murine anti-warm anti-murine anti-Ras monoclonal antibody response. This sequence encodes a method of the invention method of the invention.

Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;

9 1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAAGGGCAGAGGGCCACC . М Score 293; DB 21; Length 714; Pred. No. 8.5e-81; Indels 0; Mismatches 88.8%; 94.6%; Matches 315; Conservative Local Similarity Query Match Best Local S

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180 237 300 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTCGG 360 The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. 121 ArcrocrecaAdeccaAccaAngrerraArraAreAreAreAraAraAraAreAacrocrac CAACAGAAACCAGGACAGCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT GGGATCCCAGCCAGGTTTAGTGGCAGTGGGGTCTGGGGACAGACTTCACCCTCAACATCCAT GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCAATCTAGAATCT Drug containing humanised anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy -Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand; light chain subunit; apoptosis; immunosuppressive; antiallergic; autoimmune disease; allergy; atopic; ss. Mouse humanised anti-Fas antibody related cDNA SEQ ID NO Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other; Example 4 (Preparatory); Page 77-79; 194pp; Japanese. 330 361 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393 ACGITCGGTGCTGGGACCAAGCTGGAGCTGAAA ABL45926 standard; cDNA; 714 29-MAR-2000; 2000JP-0090918. 28-MAR-2001; 2001JP-0093106. (first entry) (SANY) SANKYO CO LTD. WPI; 2002-145113/19. P-PSDB; ABB74904. JP2001342148-A. 11-DEC-2001. 26-APR-2002 ABL45926; 301 118 181 178 241 238 298 RESULT 11 ABL45926 g g ò g Š δ ò

Gaps ٠<u>.</u> 88.8%; Score 293; DB 24; Length 714; 94.6%; Pred. No. 8.5e-81; ive 0; Mismatches 15; Indels Best Local Similarity 94.6 Matches 315; Conservative Query Match

1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCCAGAGGGCCACC 60

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61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC 117
                                                                                                                                                                                                                                                  241 GGGATCCCAGCCAGGTTTAGTGGCAGTGTGGGTCTGGGACTTCACCCTCACACATCCAT 300
                                                                                                                                                                                                                                                                                                                               CCIGIGGAGGAGGAGGAIGCIGCAACCIATTACIGICAGCAAAGIAATGAGGATCCTCGG 360
                                                                                                                                                                                                                                                                                                    CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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                                                                                                                                                                           CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                         GGGATCCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                    61 GACATTGTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGCCACC
                                                                                           ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
                                                                                                                                              CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the antibody 4H5 H chain encoding nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An antibody and the nucleic acid coding the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody 4H5 H chain encoding nucleotide sequence.
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Pred. No. 9.3e-81;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                  298 ACGITCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACGTICGGIGGAGGCACCAAGCIGGAAATCAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4 antigen; anti-human; antibody; 4H5; drug;
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GACATTGTGCTCACCAATTCTCCAGCT
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nilarity 94.6%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ58663 standard; cDNA
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P-PSDB; AAY59264.
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Best Local Similarity
Matches 315; Conserv
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                                                                                                                                                                                                                                                                                     CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and
                                                                                                                                                                                                                                                                                                                GACATTGTGCTGACCCAATCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                    ATCTCCTGCAAGGCCAGCCAAAGTGTTGTTATATGATGGTGATAGTTATATGAACTGGTAC
                                                                                                                                  CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                       GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                       ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
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Human, mouse; Fas/Fas ligand system; Fas; antibody; light chain; heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic; autoimmune disease; allergy; atopy; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised anti-Fas antibody heavy chain encoding DNA SEQ ID NO 124
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Pred. No. 8.5e-81;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                      ACGITCGGIGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                       Acgricegregaegeacaccaaecregaaarcaaa 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 112-114; 154pp; Japanese.
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Best Local Similarity 94.6%;
Matches 315; Conservative
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706 cereriesasesasesarsecrecrarraererereacaaastasesasesaserses 765
          586 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC 60
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                                                                             GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
                                                                                                                                                                                                                CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
                                                                                                                                             646 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
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(ASAH ) ASAHI MEDICAL CO LTD.
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98JP-0163023.
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26-MAY-1998;
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                                                                                                                                                                  187 caacagaaaccaccacccaaacrccrcarcraricraccaccaarcragaarcr
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P-PSDB; AAYS9265.
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Search completed: January 14, 2004, 16:03:13 Job time : 171.524 secs

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GenCore version 5.1.6
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WAS musculus (house mouse)
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WAS musculus (house mouse)
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source

FEATURES

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/ cace="female flactating)"
// issue type="mammary gland"
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// lone intermed from alactating female, and was then primed
polylinker; ist strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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Cui, D. X., Zeng, G. Y., Wang, F., Xu, J. R., Ren, D. Q., Guo, Y. H., Tian, F. R., Yan, X. J., Hou, Y. and Su, C. Z.
Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after gamma-irradiation in mice World J. Gastroenterol. 6 (5), 709-717 (2000)
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Cui,D., Zeng,G., Yan,X., Li,X. and Su,C.
Cloning of mouse genes related to repairing of intestinal
epithelium of the irradiated mice by treatment with the intestinal
RNA of mice of the same strain
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19 (1), 71-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.7%; Score 249.8; DB 10
86.5%; Pred. No. 2.2e-63;
tive 0; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 ACGTTCGGTGGAGCACCAAGCTGGAAATCAAA 404
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1. .407
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/db_xref="taxon:10090"
/clone="IMAGE:1531021"
                            musculus"
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Mus musculus
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                                                                                                                                                                           /tissue_type="timor," metastatic to mammary"
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Site_2: Sall; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
dInvestigator pronstructed by Life Technologies.
177 c 157 g 148 t
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:947121
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Pred. No. 2e-63;
0; Mismatches 31; Indels 4;
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                                          /organism="Mus musculus"
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                                                                                                                              db_xref="taxon:10090"
clone="IMAGE:4009670"
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ocation/Qualifiers
                                                                                                     strain="CZECH II"
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Best Local Similarity 89.3°
Matches 293; Conservative
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BASE COUNT ORIGIN

183 221 243 281 303 341 ESI

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

AW988429 LOCUS DEFINITION

RESULT 2

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BF581989 112-DEC-2000 774 bp mRNA linear EST 12-DEC-2000 602099444F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4219426 5',
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://inage.llnl.gov
Plate: LiAMH1004 row: c column: 02
High quality sequence stop: 508.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae; Mus.
1 (bases 1 to 774)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                           1.0108
| crganism="Wiss musculus" |
| crganism="Wiss musculus" |
| crganism="Wiss musculus" |
| dr zhain="Wiss musculus" |
| db xref="taxon:10090" |
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| clone="InAAGE:4999625" |
| clone="InbHOE" (TI phage-resistant)" |
| clone="Organ: colon; Vector: pcMV-SPORT6; Site_1: Not Site_2: Sall; cloned unidirectionally. Primer: Oligo Site_2: Sall; cloned unidirectionally. Primer: Oligo Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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BF581989.1 GI:11655610
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                                                                                    Direct Submission
Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAK43734.1"
/db_xref="G1:13877294"
/translation="LGGTRFORIRIBHRRTGGRPFQLQLGPPSERVENLITLVTEIHC
RIILLHRIYUVABEICPRPTASKFGRDPGSLLGCSIDEEFGWLSWFLLEBVHKTNANII
NTFAGSAGDGGPL9
167 g 163 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 ATCTCCTGCAGAGAGCGAAAGTGTTGATAATATTGGCATTAGTTTATGAACTGGTTC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATCCCAGCCAGGTTTAGTGGCAGTGGGGACAGACTTCACCCTCAACATCCAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATCGTGCTCACCCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCCAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACAGAAACCAGGACCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 GGGGTCCCTGCCAGGTTTACTGGCAGTGGGTCTGGGACAGATTTCAGCCTCAACATATAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ccharicaacaacaarcarcarcacacrenariicicicaccaaachaacaacarcanac 95
                    3 (bases 1 to 683)
Cui,D., Zeng,G., Yan,X., Wang,F., Tian,F., Ren,D., Zhao,T., Li,X
and Su,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                        cell type="intestinal gland cell"
'note="derived from differential display PCR between
'rradiated mice with and without RNA injection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps

    .352
    /note="related to the repair of irradiation-damaged intestinal gland cells treated with RNA"
    /codon_start=2

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.2%; Score 245; DB 11; Length 683; 85.6%; Pred. No. 8e-62; ive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGITCGGIGCTGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGITICGA GGGGGACCAAGCIGAAGCIGAAA 62
                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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Matches 285, Conservative
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AA423447 Soares mammary gland NDAMG Mus musculus cDNA clone IMAGE:832492 5' sfimlar to glo-M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN); 9b:M35699 Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (20 398) Mascra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                                                           Contact: Robert Straubserg, Fn.D.
Contact: Robert Straubserg, Fn.D.
Cond Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
Cond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LiAM10989 row: g column: 03
High quality sequence stop: 748.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211
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Oligo dT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 TATCCTGCAGAGCCAGTGAAAGTGTTGATACTTAATGGCAATAGTTTTAATGTTCTGGTACC
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Pred. No. 1.7e-61;
0; Mismatches 45;
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                                          Strausberg, Ph.D.
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al Similarity 85.5%;
284; Conservative (
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602829112F1 NCI_CGAP_C024 Mus musculus CDNA clone IMAGE:4983962 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xxef="taxxon:10090"
/db_xxef="taxxon:10090"
/clone="INAGE.421946"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="wixI (GAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 204 c 185 g 175 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGGCAGAGGGCCACACTC 117
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Muses 1 to 750)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                              Email: cgapbs remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at:
http://image.llnl.gov
Plate: LLAM99801 row; g column: 11
High quality sequence srop: 723.
Lication/Qualifiers
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86.3%; Pred. No. 9.9e-62;
cive 0; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                      Unpublished
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
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                                                                                                                                 Washir-HEMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
MGE Consortium (info@image.llnl.gov) for further information.
MGI:492708
Seq primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 GGGGTCCTGCCAGGTTTAGTGCCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCAT
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Ineising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary gland"
/dev stage="4 weeks"
/lab_host="DH108"
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                                                          Waterston, R.
The Wahlu-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:832492"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .398
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ON BY73441. GITSEN full.length enriched achit male accessory axillary lymph of Mus musculus CDNA clone G630004X22 5', mRNA sequence. BY73441. GITSTA6666

BY73441. GITSTA6666

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602834422F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989053 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                        prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/dev stage="adult"
/clone_lib="RKEN full-length enriched, adult male accessory axillary lymph node" 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                   73.3%; Score 241.8; DB 1.
85.0%; Pred. No. 6.9e-61;
iive 0; Mismatches 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGITICGGIGGAGGCACCAAACTGGAAATCGAA 423
                                                                                                                   1. .643
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="G630004K22"
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 283; Conservative
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AUTHORS
TITLE
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BG966589
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A1549800
A02 bp mRNA linear EST 23-MAR-1999
ve80a03.yl Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE: 832492 5' similar to gb.M53438 IG KAPPA CHAIN PRECURSOR V-III
REGION (HTMAN); gb:M35669 Mouse Ig aberrantly rearranged
kappa-chain mRNA V-U2-C-region, (MOUSE); mRNA sequence.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I. (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
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/lab_bos="DH10B (T1 phage-resistant)"
/lab_bos="DH10B (T1 phage-resistant)"
/clone lib="MOI (GAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 &b. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This read is a RESEQUENCE of a previously sequenced mouse clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 CAACAGAAACCAGGACAGCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAA-TGAGGATCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCCAGGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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Pred. No. 2.1e-60;
0; Mismatches 41; Indels 4;
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                                                                column: 06
                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
http://image.llnl.gov
Plate: LibMilOO2 row. k column
High quality sequence stop: 801.
Location/Qualifiers
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AI549800.1 GI:4482163
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Best Local Similarity 86.5
Matches 289; Conservative
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(CGAP)

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T 3/1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                               BI107286 876 bp mRNA linear BST 26-JUN-2001
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                            through LLNL ; contact the 
) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTAATCCTGTGGAG
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                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for i
MGI:1088814
Seq primer: -40RP from Gibco.
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                                                                                                                                                                                                                                                                                                            1. .327
/organism="Mus musculus"
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Best Local Similarity 85.8
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 CAACAGAAACCAGGACAGCACCCAAACTCCTCATCTATGCTGCATCCAACAAAAGATCC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTCCTGCAAGGCCAAGGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 CCTATGGAGGAGGATGATACTACAATGTATTTCTGTCAGCAAAGTAAGGAGGTTCCTCGG 365
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 327)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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uu91c06.yl Soares mouse NMGB bcell Mus musculus cDNa clone
IMAGE:3383818 5' Similar to SW:KV3H MOUSE P01660 IG KAPPA CHAIN
V-III REGION PC 3741/TEPC 111. ;, mRNA sequence.
            <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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This read has been verified (found to hit its original self
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Pred. No. 2.4e-60;
0; Mismatches 44; Indels 3
                                                                                                                                                                                                                                                                                                                               tissue_type="mammary gland"
'dev_stage="4 weeks"
lab_host="DH108"
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                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:832492"
                            correct orientation)
Seg primer: -40RP from Gibco.
Location/Qualifiers
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85.6%;
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Matches 279; Conservative
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603303102F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5348688 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
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/clone="lMAGE:4988086"
/clone="lMAGE:4988086"
/clone lib="WINCI CGAP CG24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo caperage insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       Email: cgapbe-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://imrough the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAMI1000 row: b column: 23
High quality sequence stop: 730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .735
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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Mus musculus
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/tlssue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="nHi08"
/lab_host="nHi08"
/clone_lib="NYCI CGAP_LU29"
/note="Organ: liumy; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 735).
                                                                                          Email: cgapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrado by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at:
Plate: LiAMI1108 row: i column: 22
High quality sequence stop: 823.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ceregacadecacecaaaereerearerarerreeareeaaeeragaareeer
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Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.9e-60;
0; Mismatches 43; Indels 3;
                                Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="CZECH II"
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Best Local Similarity 85.8%;
Matches 278; Conservative
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Dubuque, T.,
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATATGATGGTGATAGTTATATG---TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 Arcricciscaeasccaeceaestraricaridaritaridecarriagritriaricaacricgirc 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GGGGTCCCTGCCAGGTTTAGTGGCAGTGTGGGTTTGGAACAGACTTCAGCCTCAAACATCCAT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GACATIGIGCIGACCCAAICICCAGCIICTIIGGCIGIGICICIAGGGCAGCGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.1%; Score 238; DB 9; Length 420; Best Local Similarity 85.3%; Pred. No. 7.3e-60; Matches 278; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:1399038"
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/strain="C57BL/6J"
                 Mus musculus (house mouse)
Mus musculus
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/mol_type="mRNA"
/strain="MNI"
/db_xref="taxon:10090"
/clone="INAGE:5348688"
/tissue_type="tumor, gross tissue"
/dev_stge="noths"
/dev_stge="bH10B"
/lab_host="DH10B"
/loce="organ: mammary, Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: mammary", Vector: pCMV-SPORT6; Site 1: Sall;
/site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uc25e04.rl Soares mammary gland NDAMG Mus musculus CDNA clone
IMAGE:1399038 5 imilar to gb:\(\tilde{N}\) to me musculus cDNA clone
IMAGE:1399038 5 imilar to gb:\(\tilde{N}\) to describe the CHAIN PRECURSOR
V-IV REGION (HUMAN); gb:\(\tilde{A}\) to describe the CAIN PRECURSOR
kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.
AI120005.1 GI:3520329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Clone distributions of column: 01
High quality sequence stop: 839.
Location/Qualifiers
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Pred. No. 7.4e-60;
0; Mismatches 49; I
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Best Local Similarity 84.4%;
Matches 281; Conservative
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Search completed: January 14, 2004, 17:46:56 Job time : 1335.6 secs

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; Sequence 1, Application US/08483636
; Patent No. 591410
; GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smitchfilme Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UM2220
CITT: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUUTRY: ALING OF FIUSBIA
STATE: PA
COUNTRY: USA
ZUE: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PENDON MISSING
COMPUTER: PENDON MISSING
COMPUTER: PAPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
FLING DATE: 07-58P-1993
RPILOR APPLICATION NUMBER: US 08/117366
FLING DATE: 17-58P-1993
RPILORION NUMBER: US 08/117366
FILING DATE: 17-58P-1993
RPILORICATION NUMBER: US 08/136783
FILING DATE: 14-67T-1993
RPILORICATION NUMBER: PCT/US/94/10308
FILING DATE: 17-58P-1993
RPILORICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-58P-1994
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: DATE
US-08-765-469-3

US-08-436-717-24

US-08-442-542-17

US-08-487-283A-19

US-08-287-169A-3

US-08-207-169A-3

US-08-207-169A-3

US-08-207-169A-3

US-08-345-122-24

US-08-34-122-24

US-08-856-24

US-08-859-93-14

US-08-859-93-14

US-08-650-262-1

US-08-650-262-1

US-08-650-262-1

US-08-650-262-1

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US-08-68-1106-56

PCT-US96-13152-1

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FILING DATE:
ATTORNATION.
NAME: Sutton, Jeffrey A.
REGISTRATION UNDERS: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEFRONE: (215) 270-5024
TELEFRX: (215) 270-5020
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
  US-08-483-636-1
    January 14, 2004, 15:55:45; Search time 40 Seconds (without alignments) 3641.411 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
                GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-491-83-1

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US-08-137-1170-32

US-08-137-1170-32

US-08-275-053-10

US-08-275-053-10

US-08-211-980-21

US-08-211-980-21

US-08-211-980-17

US-08-477-728-66

US-08-477-728-66

US-08-487-200-66

US-08-487-200-66

US-08-553-497A-17

US-08-553-497A-17

US-08-553-497A-17

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Maximum Match 100%
Listing first 45 summaries
                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                 Length 396;
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US-08-483-622-1
Sequence 1, Application US/08483632
Sequence 1, Application US/08483632
Settle No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADRESS:
                                                                                                                                                          14; Indels
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                               89.3%; Score 294.6; DB 2;
94.9%; Pred. No. 3.2e-91;
live 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 / UW2220
STREET: King of Prussia STATE: PA
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/117366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/US/94/10308
FILING DATE: 07-5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     Best Local Similarity 94.9
Matches 316; Conservative
MOLECULE TYPE: CDNA
                                    CDS
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                                  NAME/KEY:
; LOCATION:
US-08-483-636-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
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US-08-491-845-7
Squence 7, Application US/08491845
Patent No. 5773247
GENERAL INFORMATION:
APPLICANT: MARCHI, Kaauhiko
APPLICANT: BIDA, Yasuyuki
APPLICANT: SHIOSAKI, Koulchi
APPLICANT: SHIOSAKI, Koulchi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPENDENCE ADDRESSE:
ADDRESSEE: Browdy 1-2
STRRPM
                                                                                                                                                                                                                                                                                                                                                                                                    Score 294.6; DB 2;
Pred. No. 3.2e-91;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
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STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFRYX: (215) 270-5034
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
Jeffrey A.
UMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                       89.3%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.9
Matches 316; Conservative
                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                         1..396
                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-483-632-1
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61 GACATTGTGTTGACCCAATCTCCAGCTTCTTTGTCTGTGTCTTTAGGGGAGAGGGCCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGAGTTCACCCTCAACATCCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 cererecadeadeadearecrecaacerariacióreaceaagraareageareceree 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACATTGTGCTCACCAATTCTCCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATCTCCTGCAAGGCCAAGAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 Arcriccraccadeccadeccaderorrearrangeregranarrangeaecragerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 283.4; DB 3; Length 393;
Pred. No. 2.2e-87;
0; Mismatches 21; Indels 3;
     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ACGITCGGIGCIGGACCAAGCIGGAGCIGAAA 330
                                                                                                                                                                              PRIOR APPLICATION 1973.
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-A0G-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-688-1995
ATTORNEY/AGBNT INFORMATION:
NAME: Liebescheutz, Joe O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-08-17-117D-32
US-08-106 32, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAME: Liebeschutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823
TELECOMMUNICATION INFORMATION:
TELEPRAS: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.89
Matches 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-579-378A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATCTCCTGCAAGGCCAGCCAAGTGTTGATTATGATGGTGATAGTATATATGACTAGTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CAACAGAAACCAGGACAGCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGATCCCAGCCAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CCTGTGGGAGGAGGATGGTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCGTGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGT---TGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 dedarcccaeccaecriracrescaeresercreseacaecrireaccricaacarecer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 13, Application US/08579378A
| Patent No. 6210671
| GENERAL INFORMATION:
| APPLICANT: Co. Man Sung
| TITLE OF INVENTION: Humanized Antibodies Reactive with
| TITLE OF INVENTION: Humanized Antibodies Reactive with
| TITLE OF INVENTION: Leslectin
| NUMBER OF SEQUENCES: 20
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend and Crew
| STREET: One MarketPlaza, Steuart Tower, Suite 2000
| CITY: San Francisco
| STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ee-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGTTCGGTGGAGGCACCAAGCTGGAAACTAAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                           PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN.1993
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, ROGER L.
REJESTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 268-5197
TELEFAX: (202) 737-35-8
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TENGRAL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-579-378A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-491-845-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
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177 240 237

Gaps

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238 CCTGTGGAAGAAGAAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAAGATCCTCCC 297
                                                                                                             301 cereresassersardareriscaacerarracisteasecaassiaarsassareeree 360
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                                                                                                                                                                                             RESULT 6
US-08-436-717-32
US-08-436-717-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2000-15109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REPLING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 24-APR-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR DATE: 19-FEB-1992

PRIOR DATE: 25-APR-1991

ATPORNEY/AGENT INPORMATION:

NAME: WEGNER, HAROHG 25,258

REGISTRATION NUMBER: 25,258

REGISTRATION NUMBER: 25,258

REGISTRATION NUMBER: 25,258

TELEPROMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPROMUNICATION INFORMATION:

TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 262.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Santa de la 393 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucle STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-436-717-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                            δ
                                                                                                   a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCGTGCATCCAACCTAGAATCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GACAITGIGIIGAICCAAICICCAGCIICITTIGGCIGIGICICIAGGGCAGAGGGCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATCTCCTGCAAGGCCAACCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6%; Score 262.6; DB 1; Length 3 Best Local Similarity 88.9%; Pred. No. 2.9e-80; Matches 296; Conservative 0; Mismatches 34; Indels
APPLICANT: BENDIG, MALY
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardher
ADDRESSEE: Foley & Lardher
ADDRESSEE: Foley & Lardher
                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
COUNTRY: Washington
COUNTRY: U.C.
COUNTRY: U.C.
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM FC Compatible
COMPUTER: LBM FC COMPATION
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO FCT/UP92/00544
FILING DATE: 24-APR-1992
RATOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
RATOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATOLO CKET NUMBER: 55,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
RECOMMUTICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFRAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
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LOCATION: 1..393
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STRANDEDNESS: single
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LOCATIÔN:
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181 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGTCTAGGACAGACTTCACCCTCACCATTGAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08275053

Fatent No. 5607847

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
VICUS antibody.

NUMBER OF SEQUENCE: 16
COMPUTER READABLE FORM:
MEDIUM TYPER PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION NUMBER: US/08/275,053
PRIOR SEQUENCE:
MEDIUM TYPER
SOFTWARE: PATENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
FRIOR SEQUENCE:
MINCRARIATION FOR SEQUENCE:
MINCRARI
                                                                                                                                 241 ccrerceardardardcreceaaccrarracrerceaacaaaaraardagarccecrc
                                                                        CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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                                                                                                                                                                                                298 ACGITCGGIGCTGGACCAAGCTGGAGCTGAAA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
| IENGTH: 33 base pairs | TYPE: micleic acid | STRANDEDNESS: double | TOPOLOGY: linear | MOLECTLE TYPE: CDNA to mRNA US-08-275-033-16
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Best Local Similarity 88.6%;
Matches 295; Conservative
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US-08-111-080-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
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                                                                                         1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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                                       Gaps
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TITLE OF INVENTION: virus antibody.

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC COMPATIBLE

OPERATING SYSTEM: PC CDOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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Pred. No. 9.4e-80;
0; Mismatches 35; Indels
   Pred. No. 2.9e-80;
0; Mismatches 34; Indels
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APPLICATION NUMBER: US/08/275,053
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/0179!
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-275-053-10
Sequence 10, Application US/08275053
Patent No. 5607847
GENERAL INFORMATION:
APPLICANT:
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88.6%;
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MOLECULE TYPE: cDNA to mRNA
Best Local Similarity 88.9:
Matches 296; Conservative
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Best Local Similarity 88.6
Matches 295; Conservative
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STRANDEDNESS: double
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US-08-275-053-10
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Best Local Similarity 88.6°
Matches 295; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cordregaederearearecreaecerarracrereaecaaaraareaegareceere 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CAGCAGAAACCAGGACAGCCAAACTCCTCATCTATGTTGCAACCCAAACTCCTCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACATIGIGCICACCAATICICCAGCTICITIGGCIGIGICTCTAGGGCAAGAGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
79.1%; Score 261; DB 1; Length 363;
Best Local Similarity 88.6%; Pred. No. 9.8e-80;
Matches 295; Conservative 0; Mismatches 35; Indels
                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 1111nois
                                                                                                                                                                                                      ZIP: 66606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 ACGTTCGGTGCTGGACCAAGCTGGAGCTGAAA 330
  HITLE OF INVENTION: HIV Immunotherapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGBNT INFORMATION:
NAME: BOTUM, Michael F.
REGISTRATION NUMBER: 25,447
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31
TELECHMUNICALION INFORMATION:
TELEPHONE: (312) 474-630
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 363 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25.3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-111-080-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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61 ATCTCCTGCAAGGCCAAGCCAAAGTGTTGATGATGGTGATAGTTATATG---TGGTAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.1%; Score 261; DB 1; Length 363; 88.6%; Pred. No. 9.8e-80; tive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEATCHILD: Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBTING DATA:
FLING DATA:
APPLICATION NUMBER: US/08/21,980
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AuG-1992
RADELCATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-AFR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
RESERRICE/DOCKET NUMBER: 31629
TELERFENX: (312) 474-6300
TELEFEXX: (312) 474-6448
                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: USA
                                                       GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
Sequence 21, Application US/08211980 Patent No. 5665569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25.3856
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 363 base pairs TYPE: mucleic acid STRANBEDNESS: aingle TOPOLOGY: linear MOLECULE TYPE: DNA
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181 GGGGTCCTGCCAGGTTCAGTGCCAGTGGGTCTAGGACTTCACCTCACCTTGAT 240
                                                   121 CAGCAGAAACCAGGACAGTCACGCAAACTCCTCATCTATGTTGCATCCAACCTAGAATCT 180
                                                                                               178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
                                                                                                                                                                                       238 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
                                                                                                                                                                                                                                   241 cereriogadecrearearecrecaacerarracrereaceaaaraareaeeareeeere 300
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MEDIUM TYPE: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
RROR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELERDHOME: 703-243-6430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : MILLEN, WHITE, ZELANO & BRANIGAN, P.C. 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                    298 ACGIICGGIGCIGGGACCAAGCIGGAGCIGAAA 330
                                                                                                                                                                                                                                                                                                                             301 Accircecreciedaccaacticaacticaaa 333
         118 CAACAGAAACCAGGACAGCCACCCAAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ADDA, JAUME
APPLICANT: MITJANS, FRANSEC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGER SIN
TITLE OF INVENTION: ANTI-EGER SIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08553497A Patent No. 5844093
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ADAN, JAUME
MITJANS, FRANSESC
ROSELL, ELISABET
TACO, FRANCESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENDIG, MARY M.
ANSELL, KEITH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-553-497A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARI
STATE: VI
COUNTRY:
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                                                                           181 GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTGAT 240
                                              CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 9.8e-80;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Geretein, Murray
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                   298 ACGIICGGIGCIGGGACCAAGCIGGAGCIGAAA 330
                                                                                                                                                                               301 ACGTTCGGTGCTGGACCAAGCTGGAGCTGAAA 333
                                                                                                                                                                                                                                                                                             Sequence 21, Application PC/TUS9307967
GENERAL INFORMATION:
APPLICANT: Ohno, Teuneya
TITLE OF INFORTION: HIV Immunotherapeutics
TITLE OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION
TELEPHONE: (312) 474-0448
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.6%;
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .: 363 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: 1..363
PCT-US93-07967-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                            PCT-US93-07967-21
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APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BOLUN, MICHAE! E5,447
REFERENCE/DOCKET NUMBER: 31629
TELECHONINICATION INFORMATION:
TELECHONE: (312) 474-6300
TELEFRONE: (312) 474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 6666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.0%;
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-111-080-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGGTGCATCCAAGGATCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACATTGTGCTCACCAATTCTCCAGCTTTTGGCTGTGTCTCTAGGGCAGAGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                        Score 257.8; DB 2; Length 339;
Pred. No. 1.2e-78;
0; Mismatches 37; Indels 3.
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Fatent No. 5558865
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATY APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 ACGITCGGIGCIGGACCAAGCIGGAGCIGAAA 330
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                             STRAIN: Balb/G
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: Lymph node
IMMEDIATE SOURCE:
CLONE: L3 11D (light chain)
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.0%;
Matches 293; Conservative
                         ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                    CDS
1..339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-553-497A-9
                                                                                              ORGANISM:
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61 ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGTAGTGTAT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGATCCGCTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CAGCAGAAACCAGGACAGTCACCCAAACTCCTCATCTATGTTGCATCCAACCTAGAATCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
                                                                                                                                             1 GACATTGTGCTCACCAATTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCCAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                         CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GGGTCCCTGCCAGGTTCAGTGGCAGTGTCTAGGACAGACTTCACCTCACCATTGAT
                                                                                                                                                                                                            178 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACATCCACCTCCAACATCCCAT
                                                                          Gaps
   Length 363;
                                                                      37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08211980

Sequence 17, Application US/08211980

Patent No. 566569

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya

TITLE OF INVENTION: HIV Immunotherapeutics

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun

STRET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: Chicago

STATE: Illinois

COUNTRY: Chicago
Score 257.8; DB 1
Pred. No. 1.2e-78;
0; Mismatches 37
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 19920824
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ACGITCGGIGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1931
ATTORNATION THFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31016
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELERAX: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 14, 2004, 17:48:18 Job time : 42 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 363 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1...
                                                                                     60603
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                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATATCCTGCAGAGCCAGTGAAGTGTTGATAGTTATGGCAATAGTTTTATGCACTGGTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CAGCAGAAACCAGGACAGTCACCCAAACTCCTCATCTATGTTGCATCCAACCTAGAATCT 180
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Pred. No. 1.2e-78;
0; Mismatches 37; Indels 3
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GENERAL INFORMATION:
APPLICANT: Onno, Tunneya
TITLE OF INVENTION: HTV Immunotherapeutics
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                               Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 ACGIICGGIGCIGGACCAAGCIGGAGCIGAAA 330
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                                                                                                               CLASSIFICATION: 424
RIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 9CT/US92/07111
FILING DATE: 24-ANG-1992
RIOR APPLICATION NUMBER: 9C 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY AGENT INFORMATION:
NAME: BOTHN INFORMATION:
NAME: BOTHN NUMBER: 25,447
REGISTRATION NUMBER: 25,447
REPERENCE/DOCKET NUMBER: 31629
TELEPHONE: (312),474-6300
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PETCHIIN Release #1.0, "
CUCREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEG ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.0%;
Matches 293; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1.363
US-08-211-980-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CT-US92-07111-16
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61 ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATG---TGGTAC 117
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          3;
Query Match 78.1%; Score 257.8; DB 5; Length Best Local Similarity 88.0%; Préd. No. 1.2e-78; Matches 293; Conservative 0; Mismatches 37; Indels
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US-09-759-112A-22
; Sequence 22, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
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LOCATION: (1).
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Sequence 3, Appli
Sequence 53, Appli
Sequence 51, Appl
Sequence 108, App
Sequence 108, App
Sequence 108, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Appli
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                 January 14, 2004, 16:03:20 ; Search time 196.19 Seconds (without alignments) 5928.789 Million cell updates/sec
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                                                                                                                                                                                                  US-09-759-112A-22
330
1 gacattgtgctcaccaattc......ggaccaagctggagctgaaa 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / cgn2 = 7/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/PST NEW PUB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/PSTUS PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/PSTUS PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
/ cgn2 = 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW PUB.seq:*
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version 5.1.6
- 2004 Compugen Ltd.
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US-09-759-112A-23
US-09-759-112A-23
US-10-384-933-10
US-10-216-484-10
US-10-384-933-53
US-10-316-484-53
US-10-216-484-53
US-10-216-484-53
US-10-216-484-53
US-10-216-484-108
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                                                                                                                                                                                                                                                                                                                                                  2324096 seqs, 1762381658 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                   IDENTITY NUC Gapop 10.0 , Gapext 1.0
    GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                              Sequence:
                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4297887844
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Sequence 106, App	106,	4	equence 4	equence 3	4	4	Ŋ	equence 3	equence 4	equence 4	S	'n	4	o (n	9	io	Ň	N	õ	Н	~	~	4	4	4	ñ	ĕ	ñ	m
US-10-384-933-106	-484-1	-10-384-933-4	216-484-4	-10-353-708-3	-10-353-708-4	-10-353-708-4	-10-353-7	-10-171-452A-	-10-	-10-171-452A-4	0-171-452A-	0 - 389 - 1	19-881	0 - 169 - 351 - 6	-10-169-351-6	-09-791-551-5	-10-207-655-24	-10-207-655-2	-10-207-655-26	10-027	-10-160-506	-10-160-506-7	-10-244-821-4	10-013-173-4	762-4	10-283-349-2	-10-244	-10-013-173-3	-10-150-
13	15	13	15	13	13	13	13	15	15	12	15	ď	σ		13	12	15	72	15	14	13	13	13	15	15	15	13	13	12
768	768	768	768	717	717	717	717	717	717	717	717	393	420	336	756	438	405	825	1683	809	333	333	780	780	780	394	783	783	783
		•			76.7					•	•		•										•					70.5	
	256.2			ın	10		••	10	253			-	_				-		_	-					237.6			232.8	232.8
16	17	18	19	20	21	22	23	24	25	56	27	28	5	30	31	32	33	34	35	36	37	38 U	e e	40	41	42	43	44	45

ALIGNMENTS

```
APPLICANT: Mueller, Sybille
APPLICANT: Mueller, Sybille
APPLICANT: Moleculer, Heinz
TITLE OF INVENTION: UNCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHTILE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
THER REPRENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 330; DB 11;
Best Local Similarity 100.0%; Pred. No. 8.1e-104;
Matches 330; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: 1F7 VL chain gene
US-09-759-112A-22
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: mouse
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301 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTCCG 360
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                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
RAWSCHARL RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 396;
                                                                                                                                         Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUTYER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
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Pred. No. 1.6e-91;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <UNKTOWN>
PPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
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LOCATION: 1..396
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
          Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: King of Prussia
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Best Local Similarity 94.9
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Publication US/08030100741A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Mucler, Sybille
APPLICANT: Mucler, Sybille
APPLICANT: Mucler, Sybille
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
FILE REFERENCE: 200-013
CURRENT APPLICATION NUMBER: US/09/759,112A
CURRENT FILING DATE: 2001-01-11
NUMBER OF SEQ ID MOS: 38
SOFTWARE: PATENTIN Version 3.0
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                                                                                                      ATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCT
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100.0%; Pred. No. 8.1e-104;
iive 0; Mismatches 0;
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; OTHER INFORMATION: 1F7 VL chain gene US-09-759-112A-23
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US-09-879-461-1
; Sequence 1, Application US/09879461
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Best Local Similarity 100.
Matches 330; Conservative
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US-09-759-112A-23
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LENGTH: 33
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RESULT 6
US-09-903-327A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACAGAAACCAGGACAGCCAACCCAAAGTCCTAATGCTGCATCCAATCTAGAATCT 177
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Publication No. US20030170817A1

GENERAL INFORMATION:

APPLICANT: Baruyama, No. US20030170817A1ufusa

APPLICANT: Baruyama, Hideyuki

APPLICANT: Haruyama, Hideyuki

APPLICANT: Tamaki Ikuko

CURENT: Tamaki Ikuko

FILE REFERENCE: 980126CIP/HG

CURENT PPLICATION NUMBER: US/10/384,933

CURRENT PPLICATION NUMBER: US/09/499,662

PRIOR FILING DATE: 2003-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 165

LENGTH: 714

TUDE: NUMBER OF SEQ ID NOS: 165

LENGTH: 714
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88.8%; Score 293; DB 13;
Best Local Similarity 94.6%; Pred. No. 7.3e-91;
Matches 315; Conservative 0; Mismatches 15;
298 ACGITCGGIGCTGGACCAAGCTGGAGCTGAAA 330
                                        361 ACGTICCGIGGAGGCACCAAGCIGGAAATCAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ACGITCGGIGCTGGGACCAAGCIGGAGCTGAAA 330
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US-10-216-484-10
Sequence 10, Application US/10216484
; Publication No. US20030103976A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: sig peptide
; LOCATION: (1)..(60)
US-10-384-933-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat peptide
LOCATION: (61)..(714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)..(714)
FEATURE:
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Sequence 3, Application US/09903327A

Betent No. US20020164333A1

GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGE:
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT APPLICATION NUMBER: 09/613,017
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88.8%; Score 293; DB 15;
Best Local Similarity 94.6%; Pred. No. 7.3e-91;
Matches 315; Conservative 0; Mismatches 15;
APPLICANT: Serizawa, No. US20030103976Alufusa

APPLICANT: Haruyama, Hideyuki

APPLICANT: Haruyama, Hideyuki

APPLICANT: Tawahasi, Tukuko

APPLICANT: Tawahasi, Tohru

TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG

CURRENT APPLICATION NUMBER: US/10/216,484

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US/09/499,662

PRIOR APPLICATION NUMBER: US 09/053,583

PRIOR APPLICATION NUMBER: US 09/053,583

PRIOR PILING DATE: 1998-04-01

SEQ ID NO 10

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ACGITCGGIGCIGGGACCAAGCIGGAGCIGAAA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)..(714)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (61)..(714)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: sig peptide
) LOCATION: (1)..(60)
US-10-216-484-10
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Sequence 53, Application US/10216484
Publication No. US20030103976A1
APPLICANT: Serizawa, No. US20030103976Alufusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216, 484
CURRENT PILING DATE: 2002-08-09
FRIOR PRILING DATE: 2000-02-09
PRIOR FILING DATE: 1000-02-09
PRIOR PILING DATE: 1098-04-01
NUMBER: OF SEQ ID NOS: 165
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NAME/KEY: CDS
LOCATION: (40)..(753)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (100)..(753)
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LENGIH: 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 GGGATCCCAGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCTCCAACATCCAT
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APPLICANT: Serizawa, No. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tanaki, Ikuko
APPLICANT: Tanaki, Ikuko
APPLICANT: Tanaki, Ikuko
ITILE OF INVENTION: Anti-Fes Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION WHRER: US10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION WHRER: US(09/499,662)
PRIOR APPLICATION WHRER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
LENGTH: 768
                                                                                                                                                                                                  DOCATION: (13)...(726)
CTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody US-09-903-327A-3
                                                                                                                                                                                                                                                                                          Query Match 86.8%; Score 286.6; DB 10; Length 831; Best Local Similarity 93.4%; Pred. No. 1.3e-88; Matches 311; Conservative 0; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ACGITCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 405
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 831
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Publication No. US20030170817A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat peptide
LOCATION: (100)..(753)
FEATURE:
NAME/KEY: sig peptide
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LOCATION: (40)..(753)
                                                                                                              TYPE: DNA ORGANISM: Mouse
                                                                                                                                                       FEATURE:
NAME/KEY: CDS
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159
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                                                                                                                                                                                                                                                                                                                                                                                                                                100 GACATTGTGCTCACCCAATCTCCAGGTACTTTGTCTCTGTCTCCAGGGGAGAGGGCCACC
DOCATION: (40)...(99)
FRATURE:
COTHER INFORMATION: Description of Artificial Sequence: Designed DNA
OTHER INFORMATION: encoding the light chain of humanized anti-human
COTHER INFORMATION: Fas antibody
US-10-384-933-53
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NAME/KEY: sig peptide
LOCATION: (40)..(99)
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
OTHER INFORMATION: encoding the light chain of humanized anti-human
OTHER INFORMATION: Fas antibody
US-10-216-484-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 ACGTTCGGTGCTGGACCAAGCTGGAGCTGAAA 330
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ATCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC 117
                                                                                                                                                      CAACAGAAACCAGGACAGCCAAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                                                                                                                                                   CAACAGAAACCAGGACAGGCACCCAGACTCCTCATCTATGCTGCATCCTCGAATCT 279
                                                                                                                                                                                                                                                                                                                                         CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCTTTGTAATGAGGATCCTCCC 297
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                                                                                                        160 CTCTCCTGCAAGGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Seriaawa, No. US20030170817Alufusa

APPLICANT: Seriaawa, No. US20030170817Alufusa

APPLICANT: Haruyama, Hideyuki

APPLICANT: Haruyama, Hideyuki

APPLICANT: Tamaki, Ikuko

APPLICANT: Tamaki, Ikuko

ITILE OP INVENTION: Alti-Fas Antibodies

FILE REFERRNCE: 980126CIP/HG

CURRENT APPLICATION NUMBER: US/10/384,933

CURRENT FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US/09/499,662

PRIOR APPLICATION NUMBER: EMALIER APPLICATION NUMBER: US 09/053,583

PRIOR FILING DATE: EAGL DE SERLIER FILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 165

LENGTH: 768
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US-10-384-933-108
; Sequence 108, Application US/10384933
; Publication No. US20030170817A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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LOCATION: (100) ..(753)
FEATURE:
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LOCATION: (40)..(753)
FEATURE:
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                DB 15; Length 768;
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         Query Match 83.5%; Score 275.4; DB 15; Length Best Local Similarity 91.3%; Pred. No. 9.5e-85; Matches 304; Conservative 0; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/10384933
Fublication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Harayama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Tohru
FILER REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
TENGTH: 750
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NAME/KEY: mat peptide
LOCATION: (100)..(753)
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NAME/KEY: CDS
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NAME/KEY: Sig peptide
LOCATION: (40)..(99)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haruyama, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
ITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR PILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 108
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Publication No. US20030103976A1
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LOCATION: (40)..(753)
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NAME/KEY: mat peptide
LOCATION: (100)..(753)
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NAME/KEY: sig peptide
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                      CAACAGAAACCAGGACAGCCACCCAAACTCCTCACCTATGCTGCATCCAATCTAGAATCT 177
                                                                     220 Chachgahacchggachggachcchgachcchchraigengchhchantchganch 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
ITLE OF INVENTION Anti-Fas Antibodies
FILE SEERRACE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/02/16,484
CURRENT APPLICATION NUMBER: US/09/499,662
PRIOR PILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
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NAME/KEY: CDS
LOCATION: (40)..(753)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (100)..(753)
FEATURE:
NAME/KEY: sig peptide
LOCATION: (40)..(99)
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US-10-216-484-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (13) ... (72)
O'THER INFORMATION: LIGHT CHAIN LEADER PEPTIDE
NAME/KEY: V. KEGIN
LOCATION: (73)... (405)
O'THER INFORMATION: LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19:
O'THER INFORMATION: HD37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATG----TGGTAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEX: V region
LOCATION: (454)...(825)
OTHER INFORMATION: HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19:
US-10-053-530-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                               APPLICANT: Ledbetter, Jeffrey
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Hayden-Ledbetter, Martha
APPLICANT: Hayden-Ledbetter, Martha
TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
FILE REPERENCE: 390069.401
CURRENT APPLICATION NUMBER: US/10/053,530
CURRENT APPLICATION NUMBER: US/09/765,208
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 38
SOFFWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 825
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LOCATION: (406)..(450)
OTHER INFORMATION: SYNTHETIC (GLY4SER)3 LINKER PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                          DENOM:...
DENOM:...
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC MOUSE SCFV FUSION GENE
OTHER: Misc feature
TOCATION: (13)...(72)
298 ACGIICGGIGCIGGGACCAAGCIGGAGCIGAAA 330
                            400 ACGTTCGGTCAAGCACCAAGCTGGAAATCAAA 432
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                                                                                                                                 Sequence 8, Application US/10053530 Publication No. US20030133939A1 GENERAL INFORMATION:
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Best Local Similarity 90.7
Matches 302; Conservative
                                                                                          RESULT 13
US-10-053-530-8
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RESULT 14

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NAME/KEY: V_region
LOCATION: (73)..(405)
OTHER INPORMATION: LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37
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1 LOCATION: (454)...(825)

2 OTHER INFORMATION: HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19:

US-10-207-655-8
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Sequence 8, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATICON:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Marcha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNGGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT PPLICATION NUMBER: US/10/207,655
CURRENT FILICA DATE: 202-07-25
NUMBER OF SEQ ID NOS: 426
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (406)..(450)
OTHER INFORMATION: SYNTHETIC (GLY4SER)3 LINKER PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: SYNTHETIC MOUSE SCFV FUSION GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (13)...(72)
PHER INFORMATION: LIGHT CHAIN LEADER PEPTIDE
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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HD37

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178 GGGATCCCAGCCAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACCCTCAACATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
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79.6%; Score 262.6; DB 9; Length 393;
Best Local Similarity 88.9%; Pred. No. 2e-80;
Matches 296; Conservative 0; Mismatches 34; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA 330
CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
.ENGTH: 393
; TYPE: DNA
; ORGANISM: Mus musculus
; FRATURE:
; NAME/KEY: CDS
, LUCATION: (1)..(411)
US-09-286-240-1
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January 14, 2004, 17:47:02; Search time 33.8095 Seconds (without alignments) 516.420 Million cell updates/sec
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GenCore version 5.1.6
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No. S	Score	Query	Query Match Length DB	DB	ID	Description
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7	537.5	92.4		16	AAR70189	Mouse Mab 389 1
m	537.5	92.4		20	AAY23767	Light chain vari
4	537.5	92.4		20	AAY18120	Light that a
S	532.5	91.5		21	AAY59267	Antihody 4H5 1, C
9	532.5	91.5		21	AAY51144	Murine derived n
7	532.5	91.5		21	AAY51146	Minima derived
80	532.5	91.5		21	AAY59264	Antibody 4H5 H C
σı	532.5	91.5	305	27	AAY59265	Antibody 4H5 L c

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AAY511 AAY511 AAW830 AAB147 AAW908 ABB748	AAE1837 ABG7634 AAR5512 AAR6030 AAR3212 AAP9054	AAU9985 AAP9054 AAB7189 AAW0175 AAR0413 AAR3330 AAY8519	1 AAY59263 1 AAY51140 4 AAR33305 1 AAY85193 5 AAR48618 4 ABP96773 9 AAW89333	AAB1477 AAW9092 ABB7489 ABB7493 AAW9565 AAB7693
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ALIGNMENTS

RESULT 1

A SA	ID AAO18536 standard; Protein; 110 AA. XX XX AAO18536; XX 11-OCT-2002 (first entry) XX XX XX XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; XX XX XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; XX XX XX XX XX XX XX XX XX
383	WPI; ZUUZ-590668/63. N-PSDB; AAL48661.
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New polynucleotide encoding a complementarity- or framework-determining

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Sequence 132 AA;
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07-SEP-1994;
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                                                                                                      The present invention relates to coding sequences of the murine 1F7 anti-idiotypic antibody complementarity-determining region (CDR) or framework-determining region (FR). The antibody binds to human or primate anti-human immunodeficiency virus (HIV) antibodies and can be used in the treatment of HIV infection. The present sequence is the 1F7 light chain.
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                                                                                                                                                                                                                                                                                                                                                          DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG 60
                                                                                                                                                                                                                                                                                                                        DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                                                                                                                                                                                                                                                                                       Gaps
region of an anti-idiotypic antibody that binds to human or primate anti- human immunodeficiency virus (HIV) antibodies, for use in vaccines against HIV
                                                                                                                                                                                                                                                                                                                                                                                              61 IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                      IPARFSGSGSGTDFTLNIHPVEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                  100.0%; Score 582; DB 23; Length 110; 100.0%; Pred. No. 1.3e-42; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibody; humanized antibody; antibody engineering; monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113..121
|label= CDR
|note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...20
'label= Sig_peptide
                                                                       Claim 9; Page 23-24; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR70189 standard; Protein; 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4..80
label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse MAb 3B9 light chain
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1993;
14-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9507301-A1
                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-SEP-1995
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                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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Sylvester DR;

Holmes SD,

Gross MS,

WPI; 1995-123387/16. N-PSDB; AAQ83490.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reaction;
                                                                                                            Spleen cells from mice immunized with human IL-4 were used to prepare hybridomas, which were screened for anti-IL-4 MAb secretion. Only clone 3B9 was positive. CDNA clones of the 3B9 light and heavy chains were cloned into pGSMYf+ and transformed into B. coll DHS-alpha. The clones were sequenced (AAQ83490-91), and used for
                                                                                                                                                                                                                                                                                                                                                                        1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain variable region; interleukin-4; IL-4; antibody 3B9; chimeric antibody; humanised antibody; IL-4 mediated allergic reaction Immunoglobulin E-mediated allergic reaction; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; rheumatoid arthritis; host-versus-graft disease; renal disease;
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the light chain variable region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GIPARFSGSGSGIDFILNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPPTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                     Ξ,
from high affinity mabs - useful in treatment of IL-4-mediated and igs-mediated allergic conditions
                                                                                                                                                                                                                                                                                                Score 537.5; 'DB 16; Length 132;
Pred. No. 1e-38;
1; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA molecules encoding recombinant antibodies useful treating IL4-mediated conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain variable region of murine IL-4 antibody 3B9
                                                                                                                                                                                                           antibody engineering. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sylvester DR;
                                                                               Disclosure, Fig.1, 97pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY23767 standard; Protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                  92.4%;
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93US-0117366.
93US-0136783.
94WO-US10308.
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity 93.7
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-429500/36.
N-PSDB; AAX85884.
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Gaps

1;

Length 132;

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and as such are useful in the treatment of autoimmune diseases and graft versus host disease.
                                                                                                                                                             DIVLTQSPASLAVSLGQRATISCRASQSVDYDGDSYMMWYQQRPQQPPKLLIYAASNLES
                                                                                                                                      1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                             60 GIPARFSGSGGTDFTLNIHPVEEEDAATXYCQLCNEDPPTFGAGTKLELK 110
                                                                                                         5; Indels
                                                                             Score 537.5; DB 20;
Pred. No. 1e-38;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                    CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 22-23; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                AAY59267 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Antibody 4H5 L chain fragment
                                                                           Query Match
Best Local Similarity 93.7%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-091351/08.
N-PSDB; AAZ58690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP11332563-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                         17-APR-2000
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                                                 Sequence
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                                                                                                                                                                                                                                                                     RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody, interleukin-4; IL4; immunoglobulin E; IgE mediated disease; allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock; cell proliferation regulator; therapy, autoimmune disease; graft versus host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the light chain of the murine 3B9 antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgB) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock. The antibodies are also useful for regulating B and T cell proliferation
                                                                                                                                                                                                                                                  1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                              21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMAWYQQKPGQPPKLLIYAASNLES
murine interleukin-4 (IL-4) antibody 3B9. The sequences are used in the production chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in the rapputic and pharmaceutical compositions for treating IL-4 mediated and Immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, rebuince into a lergic actions e.g. allergic rhinitis, remunatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                        60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                              81 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPPTFGGGTKLEIK 131
                                                                                                                                                                                                                         1;
                                                                                                                                                                                             20; Length 132;
                                                                                                                                                                              Score 537.5; DB 20; Lengtan
Pred. No. 1e-38;
                                                                                                                                                                                92.4%; Scor.
93.7%; Pred. No. 1e.
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain sequence for murine 3B9 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                              AAY18120 standard; Protein; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 24; Fig 1; 50pp; English.
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93US-0136783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant IL4 antibodies
                                                                                                                                                                                                                     Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-370482/31.
                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                132 AA;
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N-PSDB; AAX79519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY18120;
                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMMYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides an antibody having affinity to CD4 antigen. Th anti-buman CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents a L chain fragment of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.5%; Score 532.5; DB 21; Length 111; 92.8%; Pred. No. 2.3e-38; 1.ve 2; Mismatches 5; Indels 1;
81 GIPARFSGSGGTDFTLNIHPVEEEDAATYYCOOSNEDPPTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An antibody and the nucleic acid coding the antibody
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ID AAY51144 standard, Protein, 111 AA.
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differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                            Devices containing antibodies recognising CD4 or CD34 and their use for
the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel device (I) for separating cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQOSSEDPPTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.5%; Score 532.5; DB 21; Length 111; 92.8%; Pred. No. 2.3e-38; ive 2; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4 antigen; anti-human; antibody; 4H5; drug.
                                                                                                                                                                                                                                                                                                      Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 97-98; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY59264 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody 4H5 H chain sequence.
                                                                                                                                                                                                                                   (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
                                                                                                                                 99WO-JP02711,
                                                                                                                                                                      98JP-0159957.
98JP-0163023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0163034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 2000-086720/07.
N-PSDB; AAZ44232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP11332563-A.
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                                                                                                                               24-MAY-1999;
                                                                                                                                                                      25-MAY-1998;
                                                                                                                                                                                               26-MAY-1998;
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                                             WO9961629-A1
                                                                                    02-DEC-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
    Mus sp.
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                                                                                                                                                                                                                                                                                                      Ono M,
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                                                                                                                        Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIVITQSPASLAVSLGQRATISCKASQSVDYDGDSYMWWQQKPGQPPKILIYAASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.5%; Score 532.5; DB 21; Length 111; 92.8%; Pred. No. 2.3e-38; ive 2; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ono M, Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 95; 111pp; Japanese.
                                                                               Murine derived protein fragment #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine derived protein fragment #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY51146 standard; Protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                   98JP-0159957.
98JP-0163023.
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                                      31-MAR-2000 (first entry)
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Best Local Similarity 92.89
....hes 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-086720/07.
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AAY51144;
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Gaps

KASEI KOGYO KK.

(ASAH) ASAHI

26-MAY-1998;

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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel device (I) for separating cluster differentiation (CD)-positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoietic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention.
                                          216 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQQSSEDPPTFGGGTKLEIK 266
                     GIPARFSGSGGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devices containing antibodies recognising CD4 the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyamura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 80-82; 111pp; Japanese.
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                                                                                                                                                                                                                     Murine derived protein fragment #3.
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                                                                                                                           AAY51141 standard; Protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soka T, Morimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0159957.
98JP-0163023.
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                                                                                                                                                                                        (first entry)
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N-PSDB; AAZ44205
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26-MAY-1998;
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hes 103;
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                                                                                                                                                         AAY51141;
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Matches
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AAYS1142
ID AAYS13
                                                                                              RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMWWYQQKPGQPPKLLIYAASNLBS 215
                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                                                                                                                                           1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                       23 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMAWYQQKPGQPPKLLIYAASNLES
                                                                                                                  The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the H chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides an antibody having affinity to CD4 antigen. The anti-human CD4 antibody 4H5 is used for the detection of antigen and application for drugs. It is highly safe in human dose. The present sequence represents the L chain sequence of the antibody 4H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                    60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                           83 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSSEDPPFFGGGTKLEIK 133
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                                                                                                                                                                                                                             91.5%; Score 532.5; DB 21; Length 305; 92.8%; Pred. No. 6.3e-38; ive 2; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.5%; Score 532.5; DB 21; Length 305; Best Local Similarity 92.8%; Pred. No. 6.3e-38; Matches 103; Conservative 2; Mismatches 5; Indels 1;
                                                       An antibody and the nucleic acid coding the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD4 antigen; anti-human; antibody; 4H5; drug
                                                                                       Disclosure, Page 16-17; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 17-18; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY59265 standard; protein; 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody 4H5 L chain sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASAH ) ASAHI KASEI KOGYO KK
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                                                                                                                                                                                                                                                          Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-091351/08.
              WPI; 2000-091351/08
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                 305 AA;
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                              N-PSDB; AAZ58663
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                                                                                                                                                                                                                             Query Match
Best Local
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or CD34 and their use for

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82
                                                                                                                           1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                       23 DIVITQSPASLAVSLGQRATISCKASQSVDYDGDSYMMWYQQKPGQPPKILIYAASNLES
                                                                      Gaps
                                                                                                                                                                                                                                                   60 GIPARFSGSGSGTDFTLNIHPVEBEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                      .,
T
91.5%; Score 532:5; DB 21; Length 305; 92.8%; Pred. No. 6.3e-38; Indels 1; ive 2; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                               83 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQOSSEDPPTFGGGTKLEIK
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Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia; hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation; HIV infection; autoimmune disease; murine.
                                                                                                                                                                                                                                                                             Devices containing antibodies recognising CD4 or CD34 and their use for the separation of CD4 or CD34 positive cells
                                                                                                                                                                                                                                Ono M, Soka T, Morimoto I, Miyamura K;
                                                                                                                                                                                                                                                                                                        Claim 22; Page 82-84; 111pp; Japanese.
                                            Murine derived protein fragment #4
                                                                                                                                                                                                    (ASAH ) ASAHI KASEI KOGYO KK
(ASAH ) ASAHI MEDICAL CO LTD
                                                                                                                                                                          98JP-0159957.
98JP-0163023.
                                                                                                                                                        99WO-JP02711
                         31-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 103; Conservative
                                                                                                                                                                                                                                                 WPI; 2000-086720/07.
N-PSDB; AAZ44206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              305 AA;
                                                                                                                    WO9961629-A1
                                                                                                                                                        24-MAY-1999;
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26-MAY-1998;
                                                                                                                                     02-DEC-1999.
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5 This invention describes a novel device (I) for separating cluster differentiation (CD) positive cells using a recombinant (chimeric or single-chain) antibody recognising CD4 or CD34. The devices are useful for the separation of CD4 or CD34 positive cells, which is useful for the collection of hematopoletic undifferentiated cells, elimination of lymphocytes from cells to be used in bone marrow transplantation, the detection of leukemic cells and the production of medicinal compositions for the treatment of HIV infection and autoimmune diseases. This sequence represents a murine derived protein fragment which is used to illustrate the method of the invention. 1; Gaps 91.5%; Score 532.5; DB 21; Length 305; 92.8%; Pred. No. 6.3e-38; Indels 1;

1 DIVITINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES

AAW83042 standard; Protein; 238 AA. (updated)
(first entry) 25-MAR-2003 15-MAR-1999 AAW83042; RESULT 12 AAW83042

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

Anti-Fas MAb HFE7A light chain.

rheumatoid archritis, autoimmune haemolytic anaemia; myasthenia gravis, multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region; systemic lupus erythematosus, graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; apoptosis; HFB7A; autoimmune disease; Hashimoto's disease;

Mus musculus.

label= Sig_peptide 1..238 label= Mat_protein location/Qualifiers 1..131 |abel= Variable 32..238 label= Constant note= "claim 9" note= "claim 9" 113..121 /label= CDR L3 /note= "claim 9" 4..58 label= CDR_L1 4..80 label= CDR_L2 Protein Peptide Region Region Region Region Region

AU9859701-A

08-OCT-1998

98AU-0059701. 30-MAR-1998;

97JP-0082953 97JP-0169088 97JP-0276064 01-APR-1997; 25-JUN-1997; 08-OCT-1997;

SANY) SANKYO CO LID.

Hideyuki H, Hiroko Y, Jun O, Kimihisa I; O, Nobufusa S, Shin Y, Tohru T; Akio S, Hid Masahiko O,

WPI; 1998-543440/01. N-PSDB; AAV70130.

New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS

Reference Example 4; Page 189-190; 292pp; English.

This is the amino acid of the light chain of murine anti-human Fas monoclonal antibody HFE7A. CDNA (see AAV70130) encoding the light chain was obtained from HFE7A.secreting hybridoam (FERB BF-5E8)
RNA by RT-PCR (see AAV870127-28) produced by CDR grafting. These artibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting as induced apoptosis in normal calls. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, celerodara, Goodpastures syndrome, Crohn's disease, autoimmune haemolytic anaemia, sterility, myasthenia purpura gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura

238 AA;

Sequence

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The invention relates to compositions for the prevention or treatment containing an anti-Fas antibody as the active component. The anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the hight chain of the murine anti-human Fas monoclonal antibody HFETA, which is produced by hybridoma HFETA (FERM-BP-5828).
                                                                                                                                                                                                       59
                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine; complementarity determining region; CDR; human Fas;
Fas ligand; apoptosis modulator; programmed cell death;
autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
hepatitis; AlDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
                                                                                                                                                                                                                                21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMAWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                 1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                     Gaps
and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                       60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                81 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPRTFGGGTKLEIK 131
                                                                                                                                                                 ;;
                                                                                                                            Score 528.5; DB 19; Length 238; Pred. No. 1.1e-37; 1; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse anti-Fas antibody HFE7A light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 70; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  AAB14748 standard; Protein; 238 AA
                                                                                                                        90.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                              Local Similarity 92.8
Les 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-485645/43.
                                                                                          238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB14748;
                                                                                        Sequence
                                                                                                                            Query Match
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas lagand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyromimetic, antistheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic
                                                                                          59
                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                          21 DIVLTOSPASLAVSLGORATISCKASOSVDYDGDSYMNWYQOKPGOPPKLLIYAASNLES
                                                                                      1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                      Gaps
                                                                                                                                                                60 GIPARPSGSGSGTDFTLNIHPVEEDDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                      ..
H
                  Length 238;
Score 528.5; DB 21; Leus-
Pred. No. 1.18-37;
                                                                                                                                                                                                                                                                                                                                                                                                            Murine anti-Fas antibody HFE7A light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example reference 4; Page 104; 263pp; English,
                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serizawa N, Haruyama H, Nakahara K,
                                                                                                                                                                                                                                                                                                AAW90898 standard; Protein; 238 AA,
            90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0307711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0276882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0276881,
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-258930/23.
N-PSDB; AAA11547.
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1999;
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                                                    103;
                                                                                                                                                                                                                                                                                                                                      AAW90898;
            Query Match
Best Local S
                                                    Matches
                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                              AAW90898
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lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgan's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral inhibit apoptosis in normal cells but selectively induce it in abnormation bit obcth human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine artibes sequence represents a murine atti-fas monoclonal antibody response. This sequence represents a murine atti-fas monoclonal antibody HFE7A light chain described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 method of the invention.
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238 AA; Sequence

٦, DIVLTQSPASIAVSLGQRATISCRASQSVDYDGDSYMNWYQQRPGQPPKLLIYAASNLES 80 1 DIVLTINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59 1; Gaps 60 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQLCNEDPPTFGAGTKLELK 110 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQQSNEDPRTFGGGTKLEIK 131 Score 528.5; DB 21; Length 238; Pred. No. 1.1e-37; 1; Mismatches 6; Indels 1; 1; Mismatches 90.8%; Matches 103; Conservative Local Similarity 21 Query Match 셤 à d

ABB74867 standard; Peptide; 238 AA.

ABB74867;

26-APR-2002 (first entry)

Humanised anti-Fas antibody related peptide SEQ ID NO 33.

Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand; light chain subunit; apoptosis; immunosuppressive; antiallergic; autoimmune disease; allergy; atopic.

Homo sapiens

JP2001342148-A.

11-DEC-2001.

28-MAR-2001; 2001JP-0093106

29-MAR-2000; 2000JP-0090918.

(SANY) SANKYO CO LID.

WPI; 2002-145113/19.

Drug containing humanised anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy -

Example 6 (Preparatory); Page 26; 194pp; Japanese.

The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune RESULT 15
ABB74867
ID XX ABB74
XX ABB74
XX ABB74
DT 26-AP
XX Human
XX ABB74

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                                                                                                                                                                                                     21 DIVLIQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                       1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPFKLLTYAASNLES
                                                                                                                                  1; Gaps
diseases, allergy, atopy and others. The present sequence is that of peptide, useful to the invention.
                                                                                                                                                                                                                                                60 GIPARFSGSGSGIDFILNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                      81 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPRTFGGGTKLEIK 131
                                                                                             DB 23; Length 238;
                                                                                           Score 528.5; DB 23; Length
Pred. No. 1.1e-37;
1; Mismatches 6; Indels
                                                                                         90.8%;
                                                                                       Query Match
Best Local Similarity 92.84
Matches 103; Conservative
                                                         238 AA;
                                                         Sequence
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Search completed: January 14, 2004, 19:11:26 Job time : 35.8095 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 14, 2004, 19:02:07; Search time 14.7619 Seconds (without alignments) 716.612 Million cell updates/sec

US-09-759-112A-24 582 1 DIVLTNSPASLAVSLGQRAT......CQLCNEDPPTFGAGTKLELK 110

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: Pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	r V diedo edde PII	d kappa cha	d kappa chain V	g kappa cha	d kappa chain pr	d kappa chain V	q kappa chain	q kappa chain V	d kappa chain V	d kappa chain V	d kappa chair	the transfer of the transfer of	Id kabba chain V r	v riedo entesto	Tricks chart	rappe	s kanna chain v	a light chain or	1 , >	onoclonal antibo	kanna chain nr	chain V	kanna chain w	kanna chain	kanna chain V	rugga cmain v	Pappa obain W	y rappa chain v	chain
SUMMARIES	ai	KVMS83	KVMS43	KVMS08	S19971	PH1226	•	KVMS10	ដ	819976	~	S09966	KVMS75	KVMS40	KVMS84	S45715	KVMS37	KVMS85	855027	A56169	JC5810	KVMSM6	S68241	359	9	966	572	VMSB	34	\$26344
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Id kappa chain V r	To kappa chain V r	kanna chair	kappa chair	kappa chair	kappa chair	kanna chair	To kenthe chair V-I	light chair	chair		Id kappa chain V a		וט יייניי	To light thair V r	Ig kappa chain V r
KVMS54	PL0081	KVMS50	\$24288	696608	PN0446	KVMS32	596608	PH1076	PH0092	PH0093	E53285	JC5322	PH1077	PH1079	S37202
н	N	Т	7	N	N	Н	7	7	N	0	Ŋ	(7)	7	Ŋ	(7)
108	111	111	110	111	140	132	111	102	108	109	111	233	102	102	111
74.0	73.8	73.6	73.5	73.5	73.3	72.9	72.4	71.7	71.6	71.4	71.4	70.4	69.7	69.7	69.3
430.5	429.5	428.5	428	427.5	426.5	424.5	421.5	417.5	417	415.5	415.5	410	405.5	405.5	403.5
30	31	32	33	34	35	36	37	38	<u>გ</u>	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 KVMS83 IG Kappa chain V region (PC7183) - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Dte: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text change 21-Jan-2000	C.Accession: B01937; A01937 R.Neigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Nature 276, 785-790, 1978	A,Title: Rearrangement of genetic information may produce immunoglobulin diversity. A,Reference number: A93204; MUID:79073152; PMID:103003 A,Accession: B01937	A; Molecule type: protein A; Residues: 1-111 <wei></wei>	C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into l	v.v.berlaniny: immunoglobulin v region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin F;16-94/Domain: immunoglobulin homology <imm> F;23-92/Disulfide bonds: #status predicted</imm>	Query Match Best Local Similarity 94.6%; Pred. No. 2.6e-41; Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;	1 DIVLTNSPASLAVSLGGRATISCKASOSVDYDGDSYM-WYQQKPGGPPKLLTYAASNLES	DD 1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 60 Qy 60 GIPARFSGSGSGTDFTLNIHPVEREDAATYYCOLGNEDPPTFGAGTKTFFFK 110	RESULT 2 KWA943 Ig ka94a chain V region (PC7043) - mouse (fragment) C'Species: Mus musculus (house mouse)
0		liversity.		ical light (k sociate into		1,	5 5 9		

C;Date: 01-Sep-1981 #sequence revision 01-Sep-1981 #text change 21-Jan-2000
C;Accession: A01937; S42187; S42189; S42189; S42181; S42192
C;Accession: A01937; S42187; S42189; S42189; S42181; S42191; S42192
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
A;Molecule type: protein
A;Residues: 1-111 < WEIS
B;Mo, J.A.: Bona, C.A.: Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Recession: S42187
A;Molecule type: DNA

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Riweissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Len. 271-279, 1992
Schen 121, 271-279, 1992
A. Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on A. Reference number: PH1224; MUID:93077041; PMID:1446824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766; Note: this mouse sequence was hybridized and fused with a human constant region gene; Superfamily: immunoglobulin V region; immunoglobulin homology; Activotas: heterotetramer; immunoglobulin
                                                                                                                                  59
                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (CD4 mab clone M-T310 and others) - mouse (fragment) C;Species: Wns muscutius (house mouse) C;Species: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000 C;Accession: S19971; S19973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH1226
                                                                                                                                                                   1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                      Gaps
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A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
A;Cross--references: EMEL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A;Experimental source: clone M-T310
A;Accession: S19973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mENA
A; Readdudes: 1-12 cWENA
A; Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A; Experimental source: M-T404
C; Superfanily: immunoglobulin V region; immunoglobulin homology
C; Stywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IPM>
                                                                                                                                                                                                                                                   60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCOLCNEDPPTFGAGTKGELK 110
                                                                                                                                                                                                                                                                                                            61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
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          Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
   Score 523.5; DB 1;
Pred. No. 2e-40;
?; Mismatches 6;
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Pred. No. 3.6e-40;
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Best Local Similarity 90.1%; Pred. No. 3.1e-40;
Matches 100; Conservative 4; Mismatches 6
                                                               2;
sch
11 Similarity 91.9%;
102; Conservative
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90.1%;
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Residues: 1-131 <WEI>
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                              Best Local
Matches 10
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A.Residues: 1-111 <WEL>
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
Hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
P:16-94/Domain: immunoglobulin homology <IMM>
P:23-92/Disulfide bonds: #status predicted
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F;23-92/Disulfide bonds: #status predicted
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A;Reference number: A93204; MUID:79073152; PMID:103003
A;Accession: C01937
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Residues: 12-99 <MOZ>
Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
Note: V-kappa-21E; anti-collagen
Accession: 542191
                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 13-99 <MOF>
A;Cross-treferences: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A;Note: V-kappa-21E; anti-collagen
A;Accession: S42189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
X;Residues: 10-99 <MOX.
A;Cross-references: EMBL:225452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                       A;Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                          A;Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A;Note: V-kappa-21E; anti-collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:225448; NID:g407836; PIDN:CAA80935.1; PID:g407837 A;Note: V-kappa-21E; anti-collagen
A;Accession: S42188
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A;Residues: 10-99 <MOD.
A;Cross-references: EMBL:225454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A;Note: V-kappa-21E; anti-collagen
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90.6%; Score 527.5; DB 1
Best Local Similarity 92.8%; Pred. No. 8.9e-41;
Matches 103; Conservative 2; Mismatches 5
                                                                                                                    A; Molecule type: DNA
A; Residues: 12-99 < MOW>
                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
Residues: 15-99 <MOA>
                                                                                                                                                                                                                                             Accession: S42190
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P. Nockean, D. J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A.Title: Mechanisms of antibody diversity: multiple genes encode structurally related m. A.Title: Mechanisms of antibody diversity: multiple genes encode structurally related m. A.Focession: A01936
A.Accession: A01936
A.Accession: A01936
A.Molecule type: protein
A.Residues: 1-11 cMCK.
C.Complex: An immunoglobulin heteroteramer subunit consists of two identical light (karnain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1. C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Reywords: heterotetramer
F.16-94/Domain: immunoglobulin homology < IMM>
F.16-94/Domain: immunoglobulin predicted
                                                                                                                                           Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C;Accession: A01936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region (M-T413) - mouse (fragment)
C;Specise: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVLTQSPASLAVSLGQRATISCKASQSVDYTGESYMNWYQQNPGQSPK1LIYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQQSIQDPYTFGGGTKLEIK 111
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       Length 111;
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Pred. No. 1.3e-38;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Riek
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.6e-38;
4; Mismatches 8;
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S19972
Ig kappa chain V region (M-T321) - mouse (fragment)
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A;Molecule type: mRNA
A;Residues: 1-112 <WEI>
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Les 98; Conserv
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Best Local S:
Matches 98
                                 61
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region (PC7210) - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000 C.Accession: D01937, A01937 A.M. Garmaitan, L.; Loh, E.; Schilling, J.; Hood, L. Rightle: Rearrangement of genetic information may produce immunoglobulin diversity. A;Reference number: A93204; MUID:79073152; PMID:103003 A;Accession: D01997 A;Abhlecule type: protein A;Residues: 1-110 <WEI>
         1;
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                                                                                                                                                                                                                                                                                    Ig kappa chain V region (PC7769) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C;Accession: E01937; A01937
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
                                                                   21 DIVLTQSPASLFMSLGQRATISCKASQSLDYDGDSYMNWYQQKFGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNIES
                                           1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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       Gaps
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                                                                                                                                    GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                   81 GIPARFSGSGSGTDFTLNIHPVEEDAATYCQQSSEDPPFFGGGTKLEIK 131
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       6; Indels
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Pred. No. 3.8e-40;
  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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il Similarity 91.0%;
101; Conservative
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Conservative
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les 100; Conserv
100;
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Best Local S:
Matches 101
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Gaps

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A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1-111 < WEI>
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kage discussion immunoglobulin heterotetrames, such as IgA and IgM, the subunits associate into 1 c C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Seywords: heterotetramer; immunoglobulin
F;16-94/Domain: immunoglobulin homology < IMM>
F;23-92/Disulfide bonds: #status predicted
        C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;l6-94/Domain: immunoglobulin homology <IMM> F;l6-94/Domain: immunoglobulin homology <IMM> F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein A;Molecule type: protein Cassesidues: 1-111 <MBI: A;Molecule type: 1-111 <MBI: A;Molecule type: 1-111 <MBI: A;Molecule type: A;Molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (PC7940) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Typecies: Mus musculus (Douse mouse)
C;Species: Mus musculus (Douse mouse)
C;Species: Mus musculus (Douse mouse)
C;Accession: A01338
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Tile: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Reference number: A93204; MUID:79073152; PMID:103003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GVPARFSGSGSGTDFTLNIHPVEEEDAVTYYCOHSRELPPTFGGGTKLEIK 111
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                                                                                                                                                                                                                                                                                                           Score 473.5; DB 1;
Pred. No. 6.6e-36;
3; Mismatches 12;
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83.8%; Pred. No. 1.2e-35;
tive 4; Mismatches 13
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F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                           81.4%;
llarity 85.6%;
Conservative 3
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Best Local Similarity
Matches 95; Conserv
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C;Accession: 809966
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MUID:90269328; PMID:2347362
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C;Species: Mus musculus (house mouse)
C;Spacesion: B01938; A01938
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A;Fitle: Rearrangement of genetic information may produce immunoglobulin diversity.
A;Recession: B01938
A;Reference number: A93204; WUID: 79073152; PMID: 103003
A;Molecule type: protein
A;Residues: 1-111 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNIES 59
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                                                          Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
Accession: S19972
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-c;Date: 06-Feb-1995 #text_change 21-c;C;Date: 06-Feb-1995 #text_change 21-c;A;Weissenhorn, W.; Aiethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Aiethmueller, G.; Weiss, E.M.; Rieber, E.P.
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Reference number: S19972
A;Residues: 1-112 <WEI>A;Cross_references: EMBL:X65094; NID:G52290; PIDN:CAA46222.1; PID:G'Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <INM>
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A,Residues: 1-111 <REI>
A,Cross-references: BMEL:X51854; NID:955397; PIDN:CAA36147.1; Pi
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterzamer; immunoglobulin
F;16-94/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.5e-36;
1; Mismatches 15;
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85.6%; Pred. No. 5.5e-37;
iive 6; Mismatches 9;
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84.7%;
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Best Local Similarity 85.5.
Best Local Si Conservative
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Best Local Similarity
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RESULT

ઠે g ò g Matches

8 셤 ò 셤 RESULT 12

ä 59 9

Gaps

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9
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                                                                                           1 DIVLTNSPASLAVSLGORATISCKASOSVDYDGDSYM-WYQOKPGOPPKLLTYAASNLES
                                                     Gaps
                                                                                                                                                                                                      60 GIPARFSGSGSGTDFTLNIHPVEEDPATYYCQLCNEDPPTFGAGTKLELK 110
Query Match

80.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 1.9e-35;
Matches 93; Conservative 4; Mismatches 13; Indels 1
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RESULT 15
19 kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C;Accession: X65715
B;Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A. FEBS Lett. 346, 246-250, 1994
A;Fitle: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen-Fa A;Accession: S45714; MUID:94283606; PMID:8013642
A;Reference number: S45714; MUID:94283606; PMID:8013642
A;Retus: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-112 <KIM>A;Residues: 1-112 <KIM
A;Residues: 1-122 <KIM
A;Residues: 1-123 <KIM
A;Residues: 1-134 <KIM
A;Residues: 1-134 <KIM
A;Residues: 1-134 <KIM
A;Residues: 1-134 <KIM
A;Residues

Gaps ÷ DB 2; Length 112; 13; Indels Query Match 78.6%; Score 457.5; DB 2 Best Local Similarity 82.0%; Pred. No. 1.8e-34; Matches 91; Conservative 6; Mismatches 13 1 DIVLTNSPASLAVSLGGRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59 60 GIPARFSGSGSGTDFTLNIHPVERBDAATYYCQLCNEDPPTFGAGTKLELK 110 셤 ઠે

Search completed: January 14, 2004, 19:13:48 Job time : 15.7619 secs

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P04431 homo sapien
P16136 homo sapien
P01600 homo sapien
P01606 homo sapien
P01538 homo sapien
P01539 homo sapien
P0153 homo sapien
P05312 homo sapien
P05310 homo sapien
P05310 homo sapien
P05310 homo sapien
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ID KV3N MOUSE

CV3N MOUSE

STANDARD; PRT; 111 AA.

PT 21-UTL-1986 (Rel. 01, Created)

DT 21-UTL-1996 (Rel. 01, Last sequence update)

DT 15-UTL-1999 (Rel. 38, Last annotation update)

DE 15-UTL-1999 (Rel. 38, Last annotation update)

DE 15-WIL-1999 (Rel. 01, Last sequence with a sequence of knowns of knowns)

OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Communalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Musina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECURNCE.
MEDLINE=79073152; PubMed=103003;
Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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Pred. No. 1.8e-46;
0; Mismatches 5; Indels 1
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Mature 276:785-790(1978).

PIS. BO1937, KVMS83.

HSSP, PO1679, 2FBJ.

INTERPRO; IPRO03106, Ig_MHC.

INTERPRO; IPRO03506, Ig_WHC.

INTERPRO; IPRO03506, Ig_V.

Pfam, PP00047, ig; 1.

PROSITE; PSC0835; IG_LKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.78;
94.68;
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Best Local Similarity 94.6
Matches 105; Conservative
     129
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1108
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  KV3M MOUSE
ID KV3M MOUSE
AC P01665;
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                                                                                                                                                                                                                                                                                              DIVLINSPASLAVSLGQRAT......CQLCNEDPPTFGAGTKLELK 110
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               5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      127863 seqs, 47026705 residues
               GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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KV3H_MOUSE
KV3H_MOUSE
KV3H_MOUSE
KV3H_MOUSE
KV3T_MOUSE
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        protein search, using sw model
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KV3H_HUMAN
KV1M_HUMAN
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                               score:
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Perfect
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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                 60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                     61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                          Score 523.5; DB 1; Length 111;
Pred. No. 1.8e-45;
2; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 520.5; DB 1; Length 111;
Pred. No. 3.6e-45;
                                                                                       FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-1.
                                                                       COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                         7A4ADE4D6C256D29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region PC 7769.
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BY SIMILARITY.
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12071 MW;
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HSSP; P80362; IWTL.
InterPro; IPR003101; IG-like.
InterPro; IPR003006; IG-MHC.
InterPro; IPR003596; IG-V.
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SMART; SM00406; iGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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91.0%;
                                                                                                                                                                                                                                           89.9%;
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 276:785-790(1978).
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Matches 101; Conservative
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                                                                                                                                                                                                            111 AA;
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Best Local
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KV3Q_MOUSE
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                                                                           Eukaryota, Metroca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E., "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 527.5; DB 1; Length 111; Pred. No. 7.2e-46; 2; Mismatches 5; Indels 1
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FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7A5FCB586C306D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Rappa chain V-III region PC 6308.
Mus musculus (Mouse).
                21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region PC 7043.
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                                                                                                                                                                                                                                                   PIR, A01937; KYMS43.
HSSP; P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003596; Ig W.C.
SMART; SM00406; Ig, 1.
PROSITE; PSS0835; IG_LIKE; 1.
IRMUNDGIObulin V region.
 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12002 MW;
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InterPro; IPR07110; Ig-11ke.
InterPro; IPR003066; Ig MHC.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; ig; 1.
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Nature 276:785-790(1978).
PIR; C01937; KVMSO8.
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Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                      Nature 276:785-790(1978).
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                                                                     Mus musculus (Mouse)
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111 AA;
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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
"related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYBLOWA PROTEIN.
HSSP, P801936; KUMSCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVLTQSPASLAVSLGQRATISCKASQSVDYTGESYMNWYQQNPGQSPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 503.5; DB 1; Length 111;
Pred. No. 1.8e-43;
2; Mismatches 9; Indels 1
                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                           11964 MW; E2B1AD98AD965962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
115 Kappa chain VIII region PC 7175.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                             FRAMEWORK-1
                                                                                                                                                                                                                                                                                                 FRAMEWORK-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diversity.";
Nature 276:785-790(1978).
Nature 276:785-790(1978).
HSSP, B01679, 2FBJ.
Interpro; IPR007110; Ig-like.
Interpro; IPR03306; Ig_MHC.
Interpro; IPR033596; Ig_V.
                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR0030596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                         86.5%;
89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PP00047; ig; 1:
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin v region.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.2.,
Local Similarity 89.2.,
Local 99, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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33
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111
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93
102
23
111
111 AA;
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344
61
61
93
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P01671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Was Musculus (Mouse).
Wasaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
         60 GIPARFSGSGSGIDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                      MEDLINE=79073152, PubMed=103003,
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                             61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCHQ -SEDPWTFGSGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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Pred. No. 1.2e-43;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                      21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1986 (Rel. 38, Last annotation update)
15-JUJ-199a chain V-III region PC 7210.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain VIII region CBPC 101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-4.
BY SIMILARITY.
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SEQUENCE.
MEDLINE=79012520; PubMed=99744;
                                                                                                                                                                                                                                                                                                                                                           PIR; D01937; KVMS10.
HSSP; P01679; 2FBJ.
InterPro; IPR07110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_W
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00047; ig; 1.
SMART, SM00406, IGv. 1.
PROSITE, PS50835, IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%;
                                                                                                                                                                                                                                                                                                                                                   Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100; Conservative
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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53
60
100
110
92
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SMART; SM00406; IGV
PROSITE; PS50835: To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AA;
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                                                                                                               KV3P MOUSE
                                                                                                                                                                                                                                                                                                                                       diversity."
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-III region PC 6684.
Mus musculus (Mouse).
                                                                                                                                                                                                                                      HSSP, P80362, 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR0040; ig; 1.
PR031TE; P850835; IG_LKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.5%;
                                                                                                                                                                                                           Nature 276:785-790(1978).
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111 AA;
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                                                                                                                   1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                           60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                        61 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELFLTFGAGTKLELK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GIPARFSGSGSGTDFTLAIHPVEEEDAATYYCOLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPARFSGSGSGTDFTLNIHPVEEEDAVTYYCOHSRELPPTFGGGTKCLEIK 111
                                                                                        ι;
                                                          81.4%; Score 473.5; DB 1; Length 111; 85.6%; Pred. No. 1.7e-40; ive 3; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 470.5; DB 1; Length 111;
Pred. No. 3.4e-40;
4; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
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              111
12010 MW; F041E89AA7858523 CRC64;
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                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 7940.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                    111 AA
                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
 BY SIMILARITY
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InterPro, IPR007110, Ig-like.
InterPro, IPR03006; Ig_MHC.
InterPro, IPR03596; Ig_V.
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83.8%;
                                          Query Match
Best Local Similarity 85.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 276:785-790(1978).
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Matches 93; Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
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23
111
111 AA;
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SMART; SM00406; IG;
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                                                                                                                                                                                                                                                                                  MOUSE
               NON TER
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DISULFID
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KV3R MOUSE
ID KV3R MOU
AC P01670;
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1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diversity: multiple genes encode structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                               MEDLINE-79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (PC 3741).
MEDILINE-390731-22; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GIPARFSGSGSGTDFTLNIHPVEBEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPRTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 468.5; DB 1; Length 111;
Pred. No. 5.4e-40;
4; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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12039 MW; 1E46988341858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region PC 3741/TEPC 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
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MEDLINE-79015220; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity; multi-
"Mechanisms of antibody diversity related mouse kappa variable regions.";
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us-09-759-112a-24.rsp

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KV3U MOUSE
P01673;
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Best Local
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KV3U MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
PIR; A93204 KWMS37.
INTERPO: PRO07110; Ig-like.
INTERPO: IPR007110; Ig-like.
INTERPO: IPR003006; Ig-WC.
Pfam; PR00047; Ig: 1.
PR081TS; PS00406; IGV; 1.
PR081TS; PS00406; IGV; 1.
PR081TS; PS0835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GIPARFSGSGSRTDFTLTINPVBADDVATYYCQQSNBDPYFGGGGTKLEIK 111
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Pred. No. 1.1e-38;
7; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-3
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC46C9D259213BE4 CRC64;
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12005 MW; 39D87619313453CB CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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InterPro; IRR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PP00047; ig; 1.

PROSITE; PS50835; IG_LKE; 1.
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Best Local Similarity
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DOMAIN
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P01663;
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                                                                                                                                                                                          1 NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFWHWYQQKPGQPPKLLIYLASNLES
                                                                                                                                              1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLIYAASNLES
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Nature 276:785-790(1978).

-! MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.

-! MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.

HSSP, PO16.79; ZPR3.

InterPro; IPR003010; Ig-like.

InterPro; IPR0030506; Ig_MHC.

InterPro; IPR0030506; Ig_WHC.

InterPro; IPR0030506; Ig_V.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG 11.

PROSITE; PS50835; IG 11
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                 60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                         61 GVPARFSGSGSRIDFTLIDPVEADDAATYYCQQNNEDPLIFGAGIXLELK 111
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       Length 111;
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Pred. No. 1.3e-38;
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-1,
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                                                                           12; Indels
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DB 1;
                                       1.1e-38
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
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Last annotation update)
Query Match
78.3%; Score 455.5; Best Local Similarity 82.0%; Pred. No. 1.1e
Matches 91; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10090;
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21-JUL-1986
15-JUL-1999
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ID KV3J MC
AC P01662;
DT 21-JUL-
DT 21-JUL-
DT 15-JUL-
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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131 AA;
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MEDLINE=79012520; PubMed=99744;

MCKean D.J., Bell M., Potter M.;

Mochanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                Nature 276:785-790(1978).

Nature 276:785-790(1978).

1- MSCELLAMPOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.

HSSP, PO1679; 2FBJ.

InterPro; IPR003106; Ig-NHC.

InterPro; IPR003506; Ig-V.

Pfam; PF00047; ig; I.

PR0047; ig; I.

PR0051TE; PS08035; IG ILKE; I.

Immunoglobulin V region.
                                                                                                                                                       SEQUENCE (PC 9245).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPARFSGSGSGTDFTLNIHPVEEDAATYYCOLCNEDPPTFGAGTKLELK 110
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FRAMEWORK-4.
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80.2%; Pred. No. 4.2e-38;
iive 8; Mismatches 13
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21-JUL-1986 (Rel. 01, Last sequence update)
12-UUL-1999 (Rel. 39, Last annotation update)
19 kappa chain V-III region MOPC 63 precursor.
Ig kappa chain V-III region ABPC 22/PC 9245.
Mus musculus (Mouse).
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MEDLINE=78235887; PubMed=98179;
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MEDLINE=79012520; PubMed=99744;

MCKean D.J., Bell M., Potter M.;

Medhanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

PITO. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

HIR; B90412; KVMSM6.

HSSP; P01679; 2FBJ.
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[2]
SEQUENCE OF 21-131.
SEQUENCE OF 21-131.
MCREAN D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
Biochemistry 12:760-771(1973).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Gray W.R., Dreyer W.J., Hood L.E.;
"Mechanism of antibody synthesis: size differences between mouse
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COMPLEMENTARITY-DETERMINING-1.
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-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
HSSP; P01679; 2FBJ.
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15-JUL-1999 (Rel. 38, Last annotatic
11g kappa chain V-III region MOPC 70.
Mus musculus (Mouse).
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Interpro; IRR003006; Ig_MHC.
Interpro; IRR003566; Ig_V.
Ffam; PPF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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Search completed: January 14, 2004, 19:11:51 Job time : 10 secs

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1 DIVLTNSPASLAVSLGQRAT......CQLCNEDPPTFGAGTKLELK 110
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Copyright (c) 1993 - 2004 Compugen Ltd.
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56.2	55.9	55.8	55.7	55.2	54.0	53.9	53.6	53.4	53.4	53.2	52.9	52.7	52.5	52.4	52.4	52.3	51.8	51.5	50.6	50.4	50.1	49.7	49.6	49.6	49.2	48.7	48.1	48.0
327	325.5	325	324	321.5	314	313.5	312	311	311	309.5	308	306.5	305.5	305	305	304.5	301.5	299.5	294.5	293.5	291.5	289.5	288.5	288.5	286.5	283.5	280	279.5
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	st sequence update) kappa chain variable region Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.	s O., Cotton R.G.H.; king Antibodies Expressed BJ databases.	3526 CRC64,	DB 11; Length 111; -43; 13; Indels 1; Gaps 1;	DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLIYYAASNLES 59 	GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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19,	rel. 13, rel. 23, ti-idioto). Chordata Rodentia	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Akkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G. "Definition of the Idiotope of Pterin-Mimicking Antibodies in Mammalian Cells.", Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, A7307935; AAL09419.1; ILLerPro; IPR007101, Ig-like. INTERPRO; IPR003106; Ig-MRC.	0046; 1GV; 1. PS50835; IG_LIXE; 1. 1 11 111 111 111 111 111 NA; 12046 MW;	80.3%; Similarity 83.8%; P 93; Conservative 4;	LINSPASLAVSLGORATI 	ARFSGSGSGTDFTLNIHP
T 1 0920E9 0920E9; 01-DEC-2001	01-MAR-2003 (TEMBL). Pterin-mimicking and (Fragment). Wus musculus (Mouse) Bukaryota, Metazoa, Mammalia, Butheria,	Attin J.D., lape A., "Definition of the Id "In Mammalian Cells.", Submitted (SEP-2000) EMBL, AF307935, AAL09 InterPro, IPR003306; InterPro, IPR003596; InterPro, IPR003596;	SMART; SMOO47; 1 PROSITE; PS50835 NON_TER 1 NON_TER 111 SEQUENCE 111 P	Query Match Best Local Simi Matches 93;	1 DIV	60 GIP
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MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
Infect. Immun. 68:8003-5808 (2000).
EMBL; AF206026; ARF69324:1; -.
HSSP; P80362; IWTL.
InterPro; IPR00110; Ig-like.
InterPro; IPR003106; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLESGIPARFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Homo sapiens (Human).
Mexaryota: Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934;
ML X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AADS6280.1; -
71.0%; Score 413.5; DB 11; Length 103; 77.7%; Pred. No. 1.1e-37; Live 10; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SGSGTDFSLNIHPVEEDDIAMYFCQQSRKVPWTFGGGTKLEIK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 SGSGIDFILNIHPVEEEDAATYYCOLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 103
103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;
                                                                                                                                                                                                        103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP0047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
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                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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Best Local Si
Matches 80
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09JL80;
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Q9JL80
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGI----SNYLAWYQQKPGKVPKSLIYAASTLQS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 GVPSRFSGSGSGTDFTLTISSLOPEDVATYYCOKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 GVPSRFSGSGGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107
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                                                                                                                                                                                                                                                                  4; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 60.6%; Score 352.5; DB 4; Length Similarity 61.3%; Pred. No. 5.7e-31; 68; Conservative 16; Mismatches 22; Indels
                                                                                                                                                                                  108 108
108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 11787 MW; DB5845F19724FB4E CRC64;
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EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; 1REI.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro, IPR003006; Ig_MHC.
InterPro, IPR003596; Ig_v.
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20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQXPGQSPKLLIYKVSNRF 79
DIVLINSPASLAVSLGQRATISCKASOS-VDYDGDSYM-WYQQKPGQPPKLLTYAASNLE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQQKPGKAPNLLIYAASSLOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                               59 SGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCSI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MX X. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GIPARFSGSGSGIDFTLNIHPVEBEDAATYYCQLCNEDPPTFGAGTKLELK 110
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2
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                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030813; AAH30813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 11738 MW; CO6681716C4D16F3 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).

BMSL; AR035037; AAD56273.1; -
HSSP; PO1607; IREI.

InterPro; IRR007110; Ig-like.

InterPro; IRR003506; Ig_MHC.

InterPro; IRR003596; Ig_v.

Pfan; PF00047; ig; 1.

SMART; SM00406; IGv; 1.
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NON TER
SEQUENCE
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Q8NEK1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AP035036; AAD56272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GIPDRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
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                                                                                                                                                                                                                                                                                      MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.5%; Score 346; DB 4; Length 109; 62.2%; Pred. No. 3e-30; ive 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC019760; AAH19760.1;
InterPro; IPR003006; Ig_MrC.
InterPro; IPR003596; Ig_V.
Pfam; PR0047; Ig; 2.
SMART; SM00406; IGV; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11646 MW; SF675C52EC7EE197 CRC64;
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238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
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01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P80362; 1WTL.
INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR003006; Ig-MHC.
INTERPRO; IPR003596; Ig-V.
Pfam; PP00047; Ig; 1.
SMART; SM0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
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                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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084CI6
1D 080CI
AC 084C
DT 01-M
DT 01
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SEQUENCE FROM N.A.
STRAIN=BALBIG; TISSUB=Hyperimmunized spleen;
STRAIN=BALBIG; TISSUB=Hyperimmunized spleen;
STRAIN=BALBIG; TISSUB=Hyperimmunized spleen;
STRAIN=BALBIG; TISSUB=Hyperimmunized spleen;
Innate protecolytic antibodies: Palied D-VIPase response to the D-
entantiomer of VIP and identification of L-VIPase VL domains.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF516283; AAM64201.1;
InterPro; IPR003599; IG.
InterPro; IPR0031016; IG_MRC.
InterPro; IPR003596; IG_W.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                             01-OCT-2002 (TrEMBLrel. 22, Created)
U-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPage light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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NON TER
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Q9UL83;
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            SET THE PRESENCE OF THE PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 EIVMTQSPATLSVSPGERATLSCRASQSVT---SNLAWYQQTPGQSPRLVIYGASSRASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCOLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ-SYSTLTFGGGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINES-8875893; PubMed=9712075; MEDLINES-88375893; PubMed=9712075; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.7%; Score 341.5; DB 4; Length 234; 60.0%; Pred. No. 2.4e-29; live 18; Mismatches 23; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 58.6%; Score 341; DB 4; Length 107; Local Similarity 61.3%; Pred. No. 1e-29; les 68; Conservative 18; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; ABA68785.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03596; Ig_NHC.
                                     InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfan; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
    InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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10968A9
100968A9
101-D
101-
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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                       S
                                                                                                              1 DIVLTQSPAIMSASPGEKVTITCNASSSV----SYMHWFQQKPGTSPKLWIYSTSNLAS
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE=98277139; PubMed=9614934;
MEDILINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                   60 GIPARFSGSGSGTDFTLAIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                         58.4%; Score 34v, 63.1%; Pred; No. 1.4e-29; 1ndels +1ve 12; Mismatches 23; Indels
112 112
112 AA; 11953 MW; 4716BB7FADB543ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AR035031; AAD56267.1; -.
HSSP; P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig WHC.
InterPro; IPR00396; Ig-v.
Pfan; PR0047; ig; I.
SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                  Z
                                                    Local Similarity 63.1%
les 70; Conservative
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PRELIMINARY;

RESULT 10 QBK1F2 ID QBK1F2

Paul S.;

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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVLTQSPAIMSASPGEKVTISCSASSSVSY----MYWYQQKPGSSPKPWIYRTSNLASG
                                                                  STRAIN=BALB/C; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Tagquchi H., Planque S., Karle S., Nishiyama Y., Paul S.
Zhou Y.-X., Tagquchi H., Planque S., Karle S., Nishiyama Y., Paul S.
Innate proteolytic and identification of L-VIPsee vi domains ";
Submitted (MAY-2002) to the EMBL/GenBank/DDBU databases.
InterPro; IPR001599; IG.
InterPro; IPR00110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003006; IG_MG.
SMART; SM00409; IG; I.
SWART; SM00409; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimos; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 SGIPARFSGSGSGTDFTLNIHPVEREDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.,
Strausberg R.,
Submitted (JAN-201) to the EMBL/GenBank/DDBJ databases.
EMBL, BC002035; AAH02035.1; -.
HSSP, P01679; PABJ.
RINEEPPO: IPR00710; IG-like.
RINEEPPO: IPR003006; Ig-MHC.
RINEEPPO: IPR003306; Ig-V.
R PERM, P00047; Ig-Z.
R SWART; SMO0406; IGV; I.
R PROSITE; PS00290; IG-MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.6%; Score 315; DB 11; Length 1 60.9%; Pred. No. 5e-29; Live 10; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UN-2001 (TrEMBLrel. 17, Created)
01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-UNA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.3 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.8%; Pred. No. 1.6e-28;
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Five 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS50835; IG_LIKE; 1.
NON_TER 12 112
SEQUENCE 112 AA; 12017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.9
les 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                       SEQUENCE FROM N.A
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Matches
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Q99M37
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                                                                                                                                                                    1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYMWYQQKPGQPPKLLTYAASNLESG 60
                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
Mus maculus, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPP-TFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 IPARFSGSGSGTEFTLTISSLOSEDFAIYHCQOYNSWPPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                     61 IPARFSGSGGTDFTLMIHPVEREDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                         58.2%; Score 338.5; DB 4; Length 108; 60.9%; Pred. No. 2e-29; 1.ve 16; Mismatches 24; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.6%; Score 335; DB 4; Length 109; 60.4%; Pred. No. 4.8e-29; ive 16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AR035029; AAD56255.1;
HSSP; P80362; 1WTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003896; Ig_V.
Pfam; PF00647; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09UL85
09UL85;
01-MAY-2000 (TEMBLrel. 13, '
                                          Query Match
Best Local Similarity 60.9%
Matches 67, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment)
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SEQUENCE
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Query Match

Best Loca Matches

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QBK1F3; **08K1F3**

RESULT 13
QBKLF3
LD QBKLF3
AC QBKLFP
DT 01-OC
DT 01-ND
DT 01-W
DT 01-W
DT 01-W
DT 01-W
DT 00-W

Gaps

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1 DIVITUSPASLAVSLGQRATISCKASQSVDY-DGDSYM-WYQQKPGQPPKLLTYAASNLE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SGIPARFSGSGSTOFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWPSTFGQGTKLBIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.4%; Score 334; DB 4; Length 239; Best Local Similarity 58.0%; Pred. No. 1.6e-28; Matches 65; Conservative 18; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                           Straubberg R.;
Straubberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023362; AAH22362.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-UNA-2002 (TYEMBLrel. 21, Created)
01-UNA-2002 (TYEMBLrel. 21, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                        239 AA.
                                      PRELIMINARY;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Lung;
                                    QBTCD0
RESULT 15
Q8TCD0
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Search completed: January 14, 2004, 19:13:15 Job time : 36.3333 secs

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RESULT 1
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Sequence 2, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                     January 14, 2004, 19:10:12; Search time 13:8095 Seconds (without alignments) 337.028 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Sequence 5, A Sequence 5, A
                                                                                                                                                                          582
1 DIVLTNSPASLAVSLGQRAT.......CQLCNEDPPTFGAGTKLELK 110
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Sequence
Sequence
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(GGTZ 6/prodata/2/laa/5A COMB.pep:*
(GGTZ 6/prodata/2/laa/5B-COMB.pep:*
(GGTZ 6/prodata/2/laa/6A-COMB.pep:*
(GGTZ 6/prodata/2/laa/6B-COMB.pep:*
(GGTZ 6/prodata/2/laa/RB-COMB.pep:*
(GGTZ 6/prodata/2/laa/PCTUS COMB.pep:*
(GGTZ 6/prodata/2/laa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-483-636-2
US-08-4813-65-8
US-08-45-8
US-08-466-151-6
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-466-151-2
US-08-24
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US-08-24
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US-08-483-635-58
US-08-483-635-14
US-08-483-635-14
US-08-483-635-14
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US-08-483-632-14
US-08-483-632-14
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                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                          328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                         US-09-759-112A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                          Searched:
                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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28	449.5	77.2	111	Ŋ	US-08-483-636-73	Sequence	73, Appl
29	449.5	77.2	111	~	US-08-483-632~73	-	73. Apr
30	448.5	77.1	129	4	US-09-556-605-2		2. Appli
31	447	76.8	151	4	US-09-318-786-33	Segmence	
32	446.5	76.7	120	ч	US-08-111-080-26	Segmence	
33	446.5	76.7	120	Н	US-08-211-980-26	Segmence	. Ant
34	446.5	76.7	120	Ŋ	PCT-US93-07967-26	Segments	. Ant
35	444.5	76.4	111	H	US-08-207-169A-4		4. App.
36	444.5	76.4	121	Н	US-08-111-080-18		· co
37	444.5	76.4	121	-	US-08-211-980-18		18. Appl
38	444.5	76.4	121	വ	PCT-US92-07111-17		7. Apr
39	444.5	76.4	121	Ŋ	PCT-US93-07967-18		8. Appl
40	444	76.3	110	Н	US-08-017-570-2		P.
41	444	76.3	110	Н	US-08-471-426-2		
42	444	76.3	110	4	US-09-672-609-13	Segmence	3 Appl
43	444	76.3	110	4	US-09-025-403A-13	Sequence	3. Apr
44	444	76.3	110	Ŋ	PCT-US94-01709-2	Segmence 2	
45	439.5	75.5	132	~	US-08-379-057-16		· w

ALIGNMENTS

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21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                              60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

89.3%; Score 519.5; DB 1;

Best Local Similarity 91.9%; Pred. No. 1.4e-47;

Matches 102; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S: Browdy and Neimark
419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILI Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08579378A Patent No. 6210671
                                                                                                                                                                                                  Sequence 8, Application US/08491845 Patent No. 5773247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: M. TELECOMMUNICATION INFORMATION TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 737-352
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy an
STREET: 419 Seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                   1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLIYAASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                            21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                       GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPPTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                         1,
                                         Score 537.5; DB 2; Length 132;
Pred. No. 2.2e-49;
1; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 132;
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08483632
Patent No. 5928904
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
ATILLE OF INVENTION: Treatment of IL4 Antibodies Useful in TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 537.5; DB 2; Length
Pred. No. 2.2e-49;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-5EP-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-0CT-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US/94/10308
ATTORNER: O7-SEP-1994
ATTORNER: SULTON, JEFFREY A.
NAME: SULTON, JEFFREY A.
REDISTATION NUMBER: 34,028
BEBSISTATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P501
TELECOMMUNICATION INFORMATION:
TELEFHONE: (215) 270-5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 1946-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.4%;
                                      Query Match
Best Local Similarity 93.7%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.7
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-483-632-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-483-632-2
US-08-483-636-2
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1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 60
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81 GIPARFSGSGSGIDFTLNIHPVEREDAATYYCOOSNEDPPTFGGGTKLEIK 131
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                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MADDA, Hiroaki
APPLICANT: KIMACHI, Kasuhiko
APPLICANT: EDA, Yasuyuki
APPLICANT: SHOSAKI, Kouichi
APPLICANT: SATOSAMI, Kouichi
APPLICANT: TOKIYOSHI, Kayoshi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,845
FILING DATE:
CLASSIPICATION: 435
PRICR APPLICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00039
FILING DATE: 14-JAN-1933
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Rocce
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COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6.32509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0/18PCIDI NG/08/466,163B
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR PAPLICATION NUMBER: US 08/185,899
PRIOR PLILNG DATE: 1994-01-26
PRIOR PAPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/84,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SOFTWARE: Winperin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/466163
FILING DATE: 15-MAR-1995
PRIOR APPLICATION NUMBER: 08/185899
FILING DATE: 15-MAR-1995
FILING DATE: 26-JAN-1994
FILING DATE: 107/874-1992
FILING DATE: 107/874-1992
FILING DATE: 114-ADC-1991
APPLICATION NUMBER: 07/744768
FILING DATE: 14-ADC-1991
APPLICATION NUMBER: 07/744768
FILING DATE: 14-ADC-1991
APPLICATION NUMBER: 07/744768
FILING DATE: 14-ADC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CZAJG G.
REGISTATION NUMBER: 90.044
REFERENCE/DOCKET NUMBER: P0718P2CID:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/255-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 106 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 93.4
Matches 99; Conservative
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                                                                                                                                                           94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

88.7%; Score 516.5; DB 3; Length 131;
Best Local Similarity 90.1%; Pred. No. 3.5e-47;
Matches 100; Conservative 4; Mismatches 6; Indels 1.
AFPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One MarketPlaza, Steuart Tower, Suite 2000
CITY: San Francisco
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Retentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-MG-1995
PRIOR APPLICATION NUMBER: EP 95114696.8
FILING DATE: 17-MG-1995
PRIOR APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, OGE O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
RELEPHONE: 415-326-2400
TELEPHONE: A15-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GREEL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-466-151-6
; Sequence 6, Application US/08466151
; Patent No. 6037453
; Patent No. FURNABUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 131 amino acids TYPE: amino acid
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1 DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPQQPPKLLIYAASNLES 60
                                                                                                                                                         1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
86.5%; Score 503.5; DB 3; Length 106; 93.4%; Pred. No. 6.4e-46; Live 0; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                          60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGT 105
                                                                                                                                                                                                                                                                                                                                                                                   61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCOOSNEDPFTFGAGT 106
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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                               1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPILLIYAASYLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVLINSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                                  1; Gaps
                                                                                                                                                                               60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                 61 EIPARFSGSGSGTDFTLNIHPVEEEDAATFYCOOSHEDPYTFGAGTKLEIK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 111;
       Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Patent No. 555865

GENERAL INFORMATION:

TITLE OF INVENTION: HIV Immunotherapeutics

TITLE OF INVENTION: HIV Immunotherapeutics

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.5%; Score 491.5; DB 4
88.3%; Pred. No. 1.2e-44;
tive 3; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT PAPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-03-16
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
NUMBER OF SEQ ID NOS: 64
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08466163B Patent No. 6329509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                   US-08-466-163B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-466-163B-2
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                                                                                                                                                                                                                                                                                           1 DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 60
                                                                                                                                                                                                                                                 1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                      1;
                                                                                                                                               Score 503.5; DB 4; Length 106;
Pred. No. 6.4e-46;
0; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
                                                                                                                                                                                                                                                                                                                                                   60 GIPARFSGSGSGTDFTLNIHPVEREDAATYYCQLCNEDPPTFGAGT 105
                                                                                                                                                                                                                                                                                                                                                                                                61 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPFTFGAGT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 491.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
FILING DATE: 08-Jun-1995
FILING DATE: 15-MAR-1995
FILING DATE: 15-MAR-1995
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA: 07/874768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig 6.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 90,018PY
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    86.5%;
93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE .... 111 amino acids
TYPE: Amino Acid
TOPOLOGY: 1.4-C
                                                                                                                                         Query Match
Best Local Similarity 93.49
Matches 99, Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                             TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94080
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                                                                                                  US-08-466-163B-6
SEQ ID NO 6
LENGTH: 106
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1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMMWYQQKPGQPPKLLIYAASNVES 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLEL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GIPARFYGSGSGTDFTNTIHPVEEDDATYYCQQSIDDPSTFGGGTKLEI 110
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                     84.3%; Score 490.5; DB 1; Length 1
87.3%; Pred. No. 1.7e-44;
Live 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STREET: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTATION NUMBER: 25,447
REFERENCE/OCCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             REGISTATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 3167
REFERENCE/DOCKET NUMBER: 3167
RELECOMMUNICATION INFORMATION: TELEFONE: (312) 474-6300
TELEFONE: (312) 474-0448
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE : amino acids
                                                                                                                                                                                                                                                              LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.3 Matches 96, Conservative
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein
PCT-US93-07967-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

84.3%; Score 490.5; DB 1; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1
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Patent No. 5665569
GENERAL INFORMATION:
APPLICANT: Chno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 APPLICATION DATA: DS/08/211,980 FILING DATE: US/08/211,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
APPLICATION NUMBER: 08/111,080
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AuG-1991
PRIOR APPLICATION DATA:
APPLICATION DATA: 24-AuG-1992
PRIOR APPLICATION DATA: 24-AuG-1993
APPLICATION NUMBER: PCT/US92/07111
PRIOR APPLICATION DATA: 22-APR-1993
ATTORNEY/AGBNT TYPORMATION:
NAME: BOTUM, MIChael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCAFT NUMBER: 31629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPHONE: 25-3856
INFORMATION FOR SEG ID NO: 24: SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-111-080-24
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US-08-211-980-24
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Sequence 5. Application US/09296005
Patent No. 6290957
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER PRILING DATE: 1999-04-21
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                     1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPILLIYAASYLGS
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                                                                                                                                                                                                                                                                                       Query Match

83.4%; Score 485.5; DB 3; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/08483636
Patent No. 5914110
GENERAL INFORMATION.
APPLICANT: Gross, Mitchell S.
APPLICANT: Sylvester, Daniel R.
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SmithKline Beecham Corp./Corporate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SmithKline Beecham Corp./Corporate
Intellectual Property
O. Box 1539 / UW2220
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Pred. No. 5.3e-44;
3; Mismatches 10
                                                : 1998-06-30
UMBER: US 60/051,554
1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 83.4%;
l Similarity 87.4%;
97; Conservative
FILE REFERENCE: P1123R1
CURRENT APPLICATION WUMBER: US
CURRENT FILING DATE: 1998-06-
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        King of Prussia
                                                                                                                                                                                         TYPE: PRT
COGANISM: Mus musculus
US-09-109-207C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Mus musculus
US-09-296-005-5
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Best Local Similarity
Matches 97; Conserv
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US-09-296-005-5
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptide
                                                                                                                                                                                                                                                                                                                                                                   Sequence 5. Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                             1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
                                                                                                                                                             1 DIVLTQSPASLAVSLGQRATISCKASOSVDYDGDSYMNWYQQKPGQPPKLLIYAASNVES 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQLTQSPASIAVSIGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPILLIYAASYLGS 60
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                                                                                                                                                                                                        60 GIPARFSGSGSGTDFTLNIHPVEREDAATYYCQLCNEDPPTFGAGTKLEL 109
                                                                                                                                                                                                                                         61 GIPARFYGSGSGTDFTNTIHPVEBEDAATYYCQQSIDDPSTFGGGTKLEI 110
                         Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
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87.4%; Pred. No. 5.3e-44;
tive 3; Mismatches 10;
                         DB 5;
                 ch 84.3%; Score 490.5; DB 5
1 Similarity 87.3%; Pred. No. 1.7e-44;
96; Conservative 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-109-207C-5
; Sequence 5, Application US/09109207C
; Patent No. 6172213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 111 amino acids
Amino Acid
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Best Local Similarity 87.49
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-887-352B-5
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                    Query Match
Best Local S
Matches 96
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80.7%; Score 469.5; DB 2; Length 131; 80.2%; Pred. No. 3.1e-42; tive 8; Mismatches 13; Indels 1
ZIF: 19406-0939

COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/11/366
FILING DATE: 07.SEP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136/783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07.SEP-1994
ATTOMENYAPA/AGENT INFORMATION:
NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-636-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.23
Matches 89; Conservative
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60 GIPARFSGSGGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110

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1; Gaps

Search completed: January 14, 2004, 19:14:24 Job time : 14.8095 secs

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Sequence 24, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 115, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 54, Appl
Sequence 54, Appl
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                                                                                               January 14, 2004, 19:13:23; Search time 153.81 Seconds (without alignments) 146.239 Million cell updates/sec
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                                                                                                                                                                                           582
1 DIVLTNSPASLAVSLGQRAT......CQLCNEDPPTFGAGTKLELK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/USO6_PUBCOMB.pep:*
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9: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
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19: /cgn2_6/prodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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0 US-09-879-461-2
2 US-10-316-331-31-1
5 US-10-316-484-11
0 US-09-903-327A-4
5 US-10-194-75-115
US-09-802-096-6
US-09-802-096-6
1 US-09-802-077-2
US-09-802-077-2
US-09-802-077-2
US-09-802-077-2
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US-10-160-506-81
US-10-384-933-54
US-10-216-484-54
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                                                                                                                                                                                                                                                                                                    762491 seqs, 204481190 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                           US-09-759-112A-24
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12211
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                 Copyright
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Match 1
                                                                                                                                                                       Title:
Perfect score:
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                                                                OM protein
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                                                                                                                                                                                                                Sequence:
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RESULT 1

US-09-759-112A-24

i Sequence 24, Application US/09759112A

i Sequence 24, Application US/09759112A

i Sequence 24, Application US/09759112A

i Publication No. US20030100741A1

i GENREAL INFORMATION:

i APPLICANT: Maller, Sphile

i APPLICANT: Mohler, Helia

i TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE

i TITLE OF INVENTION: ANTIBODIES

i TITLE OF INVENTION: ANDIBODIES

i TITLE OF INVENTION: AND INTENDIFE AND INTENDIFE AND INTENDIFE ANDIBODY MATCHER AND INTENDIFE AND INTENDIFE ANDIBODY MATCHER ANDIBODY MATCHER ANDIBODY A
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Sequence 2, Application US/09879461; Publication No. US20020193575A1

RESULT 2 US-09-879-461-2

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Gaps

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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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    PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.8%; Score 528.5; DB 12; Length 238; Best Local Similarity 92.8%; Pred. No. 8.8e-44; Matches 103; Conservative 1; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berizawa, No. US20030103976Alufusa APPLICANT: Baruyama, Hideyuki APPLICANT: Maruyama, Hideyuki APPLICANT: Nakahara; Kaori APPLICANT: Tamaki, Ikuko APPLICANT: Tamaki, Ikuko APPLICANT: Tamaki, Ikuko ITLE OF INVENTION: AALI-Fas Antibodies FILE REFERNCE: 980126CIP/HG FILE REFERNCE: 980126CIP/HG CURRENT FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR APPLICATION NUMBER: US/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-10-216-484-11
Sequence 11, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 92.8%;
Matches 103; Conservative
                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
92.4%; Score 537.5; DB 10; Length 132;
Best Local Similarity 93.7%; Pred. No. 6.1e-45;
Matches 104; Conservative 1; Mismatches 5; Indels 1;
                                  APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220
Swedland Rd.
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: «UNATION»
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELEFAX: (215) 270-5090
N FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-879-461-2
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Sequence 4, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Lit, Ergansang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGE.
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
                                                                                                                 23
                                                                                                              1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
                                                          Gaps
                                                                                                                                                                                                                          60 GIPARFSGSGSGIDFILMIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                               GIPARFSGSGSGTDFTLMIHPVEEEDAATYYCQQSNEDPRTFGGGTKLEIK 131
                                                          1;
Score 528.5; DB 15; Length
Pred. No. 8.8e-44;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                          -09-903-327A-4
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Sequence 11, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
ITILE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIF/HG

CURRENT APPLICATION NUMBER: US/10/384,933 CURRENT FILING DATE: 2003-02-05 PRIOR APPLICATION NUMBER: US/09/499,662

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIVLTOSPASLAVSLGGRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                          ; LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody US-09-903-327A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
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Sequence 6. Application US/09802077

Batent No. US20010033842A1

GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE REFERENCE: P0/1922C202

CURRENT APPLICATION NUMBER: US/09/802,077

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 08/405,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 GIPARFSGSGSGIDFTLNIHPVEEEDAATYYCQQINEDFWIFGGGIKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIPARFSGSGSGTDFTLMIHPVEEEDAATYYCQLCNEDPPTFGAGTKLELK 110
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Query Match

Best Local Similarity 92.8%; Pred. No. 1.4e-43;

Matches 103; Conservative 1; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 112;
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88.3%; Pred. No. 6.7e-42;
iive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 115, Application US/10194975
PUblication No. US20030039649A1
PUblication No. US20030039649A1
APPLICANT: FOOTE, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: S01231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR PRILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Version 3.1
LENGTH: 112
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                               TYPE: PRT
ORGANISM: Mouse
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US-10-194-975-115
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Sequence 6, Application US/09802096

Patent No. US20010038839A1

GENERAL INFORMATION:

APPLICANT: Datdieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amender FILE REFERENCE: P0718P2C3US

CURRENT APPLICATION NUMBER: US/09/802,096

CURRENT APPLICATION NUMBER: US 08/405,617

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR PILING DATE: 1994-01-26

PRIOR PILING DATE: 1994-01-26

PRIOR PILING DATE: 1992-08-14

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR PILING DATE: 1992-06-07

PRIOR PILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 503.5; DB 9;
Pred. No. 9.9e-42;
0; Mismatches 6;
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR PRILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-05-07
NUMBER OF SEQ ID NOS: 64
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US-09-925-179-6
; Sequence 6, Application US/09925179
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93.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
US-09-802-077-6
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Best Local Similarity
Matches 99; Conserva
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Sequence 2, Application US/09802096
Patent No. US20010038839A1
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Publication No. US20030044858A1
GENERAL INFORMATION:
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CRGANISM: Mus musculus
US-09-802-096-2
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SEQ ID NO 2
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Facent No. US20010033842A1

GENERAL INFORMATION

APPLICANT: Jaxdieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US

CURRENT APPLICATION NUMBER: US/09/802,077

CURRENT PILING DATE: 2001-03-08

FRIOR FILING DATE: 1995-03-15

PRIOR PPLICATION NUMBER: US 08/185,899

FRIOR APPLICATION NUMBER: PCT/US92/06860

PRIOR PPLICATION NUMBER: PCT/US92/06860

PRIOR PILING DATE: 1992-06-14

FRIOR FILING DATE: 1992-06-14

PRIOR FILING DATE: 1992-06-14

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1991-08-14

PRIOR FILING DATE: 1991-08-14
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88.3%; Pred. No. 1.5e-40;
cive 3; Mismatches 9; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 503.5; DB 11; Length
Pred. No. 9.9e-42;
0; Mismatches 6; Indels
              GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REPRENCE: P0718P2C1D1C1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
Publication No. US20030044858A1
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Best Local Similarity 93.4%;
Matches 99; Conservative
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ORGANISM: Mus musculus
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CORGANISM: Mus musculus
US-09-802-077-2
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Best Local Similarity
Matches 98; Conserva
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GENERAL INFORMATION:
APPLICANT: Dardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Dardieu, Paula M.
APPLICANT: Dardieu, Paula M.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TITLE OF INVENTION) NUMBER: US 109/802,036
CURRENT PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR PLILING DATE: 1992-08-14
PRIOR PLILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/844,768
PRIOR APPLICATION NUMBER: US 07/744,768
1 DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPILLIYAASYLGS 60
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Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1.
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended);
FILE REPERENCE: P0718P2C1D1G1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT PILING DATE: 2001-08-08
PRIOR PRILING DATE: 1995-06-06
PRIOR PRILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-08-14
PRIOR PILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR PILING DATE: 1992-08-14
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Query Match
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| Publication No. US20030161832A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
| TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
| TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
| TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
| FILE REPERENCE: 10448-162001
| CURRENT APPLICATION NUMBER: 0/3024,100
| PRIOR FILING DATE: 2001-09-20
| PRIOR PILING DATE: 2001-09-20
| PRIOR FILING DATE: 2002-03-08
| NUMBER OF SEQ ID NOS: 128
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                 Length 111;
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Publication No. US20030170817A1
GENERAL INPORMATION;
APPLICANT: Serizawa, No. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahara, Kaori
APPLICANT: Takahashi, Tohru
ITIME OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 9801261P/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
FRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
FRIOR FILING DATE: 2000-02-09
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/499,662
                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%; Score 490; DB 12;
85.7%; Pred. No. 2.2e-40;
                                                                                                                            Score 491.5; DB 1
Pred. No. 1.5e-40;
3; Mismatches 9
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7; Mismatches
                                                                                                                            84.5%;
                                                                                                                                                                    Conservative
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                                        TYPE: PRT
ORGANISM: Mus musculus
US-09-925-179-2
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US-10-160-506-81
                                                                                                                      Query Match
Best Local Similarity
Matches 98; Conserv
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SEQ ID NO 2
LENGTH: 111
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Best Local S
Matches 96
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1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVLTNSPASLAVSLGQRATISCKASQSVDYDGDSYM-WYQQKPGQPPKLLTYAASNLES
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                                                                                                                                                                                 Designed light
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIPARFSGSGSGTDFTLNIHPVEBEDAATYYCOLCNEDPPTFGAGTKLELK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GIPDRFSGSGSGTDFTLTIHPVEREDAATYYCQQSNEDPRTFGQGTRLEIK 131
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                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.8%; Score 487.5; DB 15; Length 238; 83.8%; Pred. No. 8.8e-40; Indels 1;
                                                                                                                                                                                                                                                                           83.8%; Score 487.5; DB 12; Length
83.8%; Pred. No. 8.8e-40;
.ive 7; Mismatches 10; Indels
                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: chain of humanized anti-Fas antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: chain of humanized anti-Fas antibody
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 54
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-215

Sequence 54, Application US/10216484

Publication No. US20030103976A1

GENERAL INFORMATION:

APPLICANT: Serizawa, No. US20030103976Alufusa

APPLICANT: Haruyama, Hideyuki

APPLICANT: Tamaki, Ikuko

APPLICANT: Tamaki, Ikuko

APPLICANT: Tamaki, Ikuko

TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR PELLING DATE: 2002-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
LENGTH: 238
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                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.8
Matches 93; Conservative
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Matches 93; Conserv
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